

DR HSP; Q9Y286; 1075.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 3.
KW Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 20
FT CHAIN 21 597
FT
FT
FT DOMAIN 21 483
FT TRANSMEM 484 504
FT DOMAIN 505 597
FT DOMAIN 21 144
FT DOMAIN 145 271
FT DOMAIN 277 360
FT DOMAIN 367 464
FT SITE 565 570
FT SITE 589 593
FT DISULFID 46 106
FT DISULFID 168 301
FT DISULFID 173 233
FT DISULFID 295 344
FT DISULFID 403 448
FT CARBOHYD 142 142
FT CARBOHYD 181 181
FT CARBOHYD 232 232
FT CARBOHYD 292 292
FT CARBOHYD 362 362
FT CARBOHYD 369 369
FT CARBOHYD 387 387
SQ SEQUENCE 597 AA; 65075 MW; 74C13CPA9CDB5BA5 CRC64;
Query Match 33.6%; Score 909; DB 1; Length 597;
Best Local Similarity 41.4%; Pred. No. 1.4e-53;
Matches 212; Conservative 70; Mismatches 164; Indels 66; Gaps 11;
QY 7 LSLGGSQAMGRFIRVOESVMVEGLICISVPCSFSPRODWTGSTPAYGYWFKAVTE 66
DB 139 LSNVTASDLSRYRLEVPESVTQGLCVSPVCSVLYPHCNVTASSPVYGSWFKEGAD 198
QY 67 TTKGAPVATNHQREVMSTRGRFQLTGDPKNCSLVIRDAQMDQESYFFRVERGSV 126
DB 199 IPDIPVATNTPSGKVEDTQGRFLLDGPDQTNCSLSIRDAKGDGSKYVQVERGS- 257
QY 127 RYFMNDGFLKYALTQKPDVYIPETLEPGQPVTVICVFNNAFECPPPPSPFSWTGAALS 186
DB 258 KWNIVDKLSVHTALTLPETSPGTLESHPNLTCSVPWACEQGTPTTITWNGASVS 317
QY 187 SQGKSTTSFSLVSPTRPDHDTLTCHVDPSRKGVAQRTVRLRAYAPRDLVISIS 246
DB 318 S--LEPTISRSMLSLIPKPDHGTSLTCQVTLPGAGVTTTAVRLNISY----- 365
QY 247 RDNTPDPENLRVMVQANRTVLENLNGTSLPVLGQSLCLVCTHSSPPARLSWTQRG 306
DB 366 -----PPQNLTWTVFGDGTASTTLRNGSALSVLEGSQSLHLCVADVSNPRLSWTWS 419
QY 307 QVLSPQSPDPGVLELPRVOVEHEGFTCHARPLGSHVSLSVHYK---KGLISTAF 363
DB 420 LTLSPSQSSLGLVLELPRVHVKEGFTCRAQNPGLSQHISLSLQNEYTGKMRPISGV 479
QY 364 SNGAFILGIGTALLFLCLALIMKILPKRRTQETPRPRFSRHTLTLDVINVY---PTAG 420
DB 480 TLGAVGAGATLVLSFCILFVVV---RSCRKKSARPAVGVDGTGMDTNAVGSASQG 536
QY 421 FLAQKRNQKATNPSRPTPLPPGAPSPESKKNQKQYCLPSFPPEPKSSTOAPESQEBEL 480
DB 537 FLI-----ESPADDSPPHHAPALATP-----FPE-----EGEI 565
QY 481 HYATLNPFGVPRPPEARMKPGTQA---DYAEV 509
DB 566 QYASLSFHKARP---QYPOEQEAGYEVSEI 593

RESULT 12

Q6PJ50 PRELIMINARY; PRT; 468 AA.
ID Q6PJ50
AC Q6PJ50;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SIGLEC-like 1.
GN Name=Siglec1;
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Heltan E., Kettman M., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC023280; AAH23280.1; -.
DR GO; GO:0004872; F:receptor activity; IDA.
DR GO; GO:0005057; F:receptor signaling protein activity; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 468 AA; 51987 MW; 26A0FF74D3CA4ACF CRC64;

Query Match 32.4%; Score 878; DB 2; Length 468;

Best Local Similarity 39.0%; Pred. No. 1.4e-51;

Matches 204; Conservative 75; Mismatches 170; Indels 74; Gaps 11;

QY 1 MLLPILLSSLLGGSQAMGR-----FWIRVOESVMVEGLICISVPCSFSPRO---DWG 52

DB 1 MLLPILLSSLLGGSQAMGR-----FWIRVOESVMVEGLICISVPCSFSPRO---DWG 52

QY 53 STPAYGYWFKAVTETTKGAPVATNHQREVMSTRGRFQLTGDPKNCSLVIRDAQMDQ 112

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61 SDPVHGFWRGTDARKDSIVATNNPIKAVKETRNRFFLLGEPWRNDCSLNIREIRKKD 120
113 ESQFFFRVERGSYRVNPNWDGFFIKVTALTOKPDWI:PETLEPQPVTVICFNWAFEE 172
121 AGLYFFRLERKQ-TKYNMWDQMTLVATLINTPOILL:PETLEAGHPSNLTCSEVDCGW 179
173 CPPPSFSWTGAALSSQGTKFTTSHESVLSPFPRPDHDTDLTCHVDHFKRGKVSQAQTVRL 232
180 TAPPIFSMTGTSVSFLSTNTTGS--SVLTITPQPDHGTINTCQVTLPGTDVSTMTIRL 237
233 RVAVAPRLDIVISIRDNTDPDENRVMVVSQANRTVLNGLNGTSLPLVGGOSLCLVCVT 292
238 NVSVAPK-----NUTVIYQADSVSILKNGSBLP:SEGOUSLELCST 281
293 HSSPPARLSWTORGQVLSQSPSDGVLELPRVQVEHEGETTCHARHPLGSHQVLSLSLV 352
282 DSYPPANLSWSDNLTLCESKLSKGLLELFPVHLKHGGVTTQQAHALGSHISLSLSP 341
353 HYKGLISTASNGAFLGIGITALLFLCLALILKILPKRQTQE---TSPRFRSHST 408
342 QSSATL--SEMMGTGTFVGGVTALEFLSVLCILLAVRSYRKRPAPVAVAPHP 392
409 ILDIVNVYPTAGPLAQRKNQKATENSPTPLPGAPSPESKKQKQYQLSPFPEPKSST 468
393 --DALKVSQSNPLVESQADDS-----SEPLPSILE 421
469 QAPSESQSQEBLHVATLNFPGVRPRPEARMPKGTQADVAEVKF 511
422 AAPSTE--EEIHVATLSFHEMKPM-NLWGOQDITTEYSEIKF 461

RESULT 13
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ID AAQ79834 PRELIMINARY; PRT: 468 AA.
AC AAQ79834;
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DE 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE Sialic acid binding immunoglobulin-like lectin-E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_taxid=10090;
[1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6;
RA Zhang J.Q., Crocker P.R.;
RT "Characterization of mSiegles-E and -F.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY348552; AAQ79834.1;
KW Lectin.
SQ SEQUENCE 468 AA; 51987 MW; 26A0FF74D3CA4ACF CRC64;

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Db 342 QSSATL--SEMMGTFFVSGVATLLFLSVCILLAVRSYRRKPARPAVAVPH-----392
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Db 393 --DALKVSVSQNPLVESQADDS-----SEPLESILE 421
QY 469 QAPESQESQEBELHYATLNFPGVRPRPEARMKPGTQADYAEVKF 511
Db 422 AAPSTE--EEHYATLSFHEMKPM-NLWGQDTTTEYSEIKF 461

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AC AAH23280;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE SIGLEC-like 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung, MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mancini P.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung, MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC023280; AAH23280.1; -. 26A0FF74D3CA4ACF CRC64;
SQ SEQUENCE 468 AA; 51987 MW; 26A0FF74D3CA4ACF CRC64;

Query Match 32.4%; Score 878; DB 2; Length 468;
Best Local Similarity 39.0%; Pred. No. 1.4e-51;
Matches 204; Conservative 75; Mismatches 170; Indels 74; Gaps 11;

QY 1 MLPLLLSSLLGGSQMDGR-----FWIRQESVMVPEGLICISVPCSFSPYPRQ---DWTG 52
Db 1 MLPLLLSSLLGGSQMDGR-----FWIRQESVMVPEGLICISVPCSFSPYPRQ---DWTG 52
QY 53 STPAYGVFWKAVTETTKGAPVATNQHOSREVEMSTRGRFQITGDPKAGNCSLVIRDAQMOD 112
Db 61 SDPVHGFWYEGTDRKDSIVATNPKRAVETRNRFLLGEPWENDCSLNIREFKRD 120
QY 113 ESQYFRVRERGSVYRNFMNDGFLKVTALTQKPDVYIPETLEPGQPVTVCVFNWAFEE 172
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Db 180 TAPFISWTGTSVSLSTNTTGS--SVLTITPQDQHGTLNLTQVTLPGTDVSTRMTIRL 237
QY 233 RVAYAPRDLVISISRDNTPOPPENLRVWVSQANRTVLENLNGTSLFVLEGGQSLCLVCVT 292
Db 238 NVSYAPK-----NLTVTIYQGADSVSTILKNGSSLPISGQSLRLICST 281
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QY 353 HYKGLISTAFSNGAFLGIGITALLFLCLALIMKILPKERTOTE---TPRPRFSRHS 408
Db 342 QSSATL--SEMMGTFFVSGVATLLFLSVCILLAVRSYRRKPARPAVAVPH-----392
QY 409 ILDYINVVPTAGPLAQKQKATPNSPRTPLPGAPSPESKQKQYQLPFPPEPKSST 468
Db 393 --DALKVSVSQNPLVESQADDS-----SEPLESILE 421
QY 469 QAPESQESQEBELHYATLNFPGVRPRPEARMKPGTQADYAEVKF 511
Db 422 AAPSTE--EEHYATLSFHEMKPM-NLWGQDTTTEYSEIKF 461

Search completed: November 5, 2004, 13:57:39
Job time : 116.542 secs
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:18 ; Search time 17.3484 Seconds
(without alignments)
1957.231 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLLPILLSLLGGSQMDGR.....RPEARMPKGTQADYAEVKFQ 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/aaa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/aaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/aaa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/aaa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/aaa/ECTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	888	32.8	431	3	US-09-038-832-4
3	831.5	30.7	467	3	US-09-046-736-2
4	800.5	29.6	551	4	US-08-896-537A-2
5	769	28.4	440	3	US-08-759-628-4
6	693.5	25.6	421	3	US-08-759-628-5
7	693	25.6	364	4	US-08-896-537A-3
8	573	21.2	374	3	US-09-046-736-4
9	346	12.8	64	4	US-09-513-999C-7159
10	200	7.4	56	4	US-09-513-999C-4599
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15	153.5	5.7	416	4	US-09-638-649-1
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18	151.5	5.6	1241	3	US-09-040-774-2
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44	132	4.9	828	1	US-08-261-304-2
45	131.5	4.9	405	4	US-08-755-235-4

ALIGNMENTS

RESULT 1

US-09-038-832-2

; Sequence 2, Application US/09038832

; Patent No. 6146845

; GENERAL INFORMATION:

; APPLICANT: KIKLY, KRISTINE

; APPLICANT: ERICKSON-MILLER, CONNIE

; TITLE OF INVENTION: Sialoadhesin Family Member-2

; TITLE OF INVENTION: (SAF-2)

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESS: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/038,832

; FILING DATE: 11-MAR-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/041,886

; FILING DATE: 02-APR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-50018

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 431 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-038-832-2

Query Match 32.8%; Score 888; DB 3; Length 431;

Best Local Similarity 47.8%; Pred. No. 1.5e-69;

Matches 195; Conservative 52; Mismatches 127; Indels 34; Gaps 6;

Patent No. 5169835
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Sequence 5, Appli
Sequence 14, Appli
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Sequence 14, Appli
Sequence 6, Appli
Sequence 84, Appli
Sequence 84, Appli
Sequence 84, Appli
Sequence 348, Appli
Sequence 84, Appli
Sequence 2, Appli
Sequence 10, Appli
Sequence 23, Appli
Sequence 2, Appli
Sequence 4, Appli

1 MLLPILLSLLGGSCAMDG-----REWIRVQSVMMVEGLCISVPCSFSPYQDWTGST 54
 1 MLLPILLSLLGGSCAMDG-----REWIRVQSVMMVEGLCISVPCSFSPYQDWTGST 60
 55 PAYGWFKAVTETTKGAPVATNHQSRVEMSTGRFOLTGDPAKNGNSLVIRDAQMODS 114
 61 PVHGYWFRAGDRPYQDAPVATNPNPDREVQAEQCFOLLGDIWSNDCSLSIRDARKRDKG 120
 115 QYFRVERGYSY-----VRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFVNA 169
 121 SYFRLERGMKWSYKQNLNKTQKLSVFTVLTALTRPDILILGLTSGHSRNLTCVFPWA 180
 170 FEECPPEFSWGTGAALSQGTPTTSHPSVLSFTPRPDQDHTDITLCHVDFSRKGVSAQRT 229
 181 CKQGTTPMISWIGASVSSPG--PTTARSSVLTLPKPDQDHTSLTQVTLPGTGVTTTST 238
 230 VRLRVAYAPRDLVISISRDNTDPPENLRVMVQANRTVLENLGNCTSLPVLEQSLCLV 289
 239 VRLDVSY-----PPMNLTVTFQGDATASTALNGSSLSVLEQSLRLV 282
 290 CVTHSSPPARLSWTQRCQVLSPPQSPDPGVLELPRVQVEHEGFTCHARHPLGSHVLSLS 349
 283 CAVNSNPPARLSWTQRCQVLSPPQSPDPGVLELPRVQVEHEGFTCHARHPLGSHVLSLS 342
 350 LSVHYKKGLISTAPSN--GAFLGIGITALLFL--CLALIIMKILPKR 392
 343 LSLQNEGTGSRPVSVQVTLAAVGGAGATATAFLSFCIIIFIIVRSCKRK 390

RESULT 2

US-09-038-832-4
 Sequence 4, Application US/09038832
 Patent No. 6146845

GENERAL INFORMATION:

APPLICANT: KIKLY, KRISTINE
 APPLICANT: ERICKSON-MILLER, CONNIE
 TITLE OF INVENTION: Sialoadhesin Family Member-2
 TITLE OF INVENTION: (SAP-2)

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: RATNER & PRESTIA
 STREET: P.O. BOX 980
 CITY: VALLEY FORGE
 STATE: PA
 COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA: US/09/038,832

FILING DATE: 11-MAR-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/041,886

FILING DATE: 02-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-50018

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 431 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-038-832-4

Query Match

Best Local Similarity 32.8%; Score 888; DB 3; Length 431;

Matches 195; Conservative 52; Mismatches 127; Indels 34; Gaps 6;

QY 1 MLLPILLSLLGGSCAMDG-----RFWRVQSVMMVEGLCISVPCSFSPYQDWTGST 54

DB 1 MLLPILLSLLGGSCAMDG-----RFWRVQSVMMVEGLCISVPCSFSPYQDWTGST 60

QY 55 PAYGWFKAVTETTKGAPVATNHQSRVEMSTGRFOLTGDPAKNGNSLVIRDAQMODS 114

DB 61 PVHGYWFRAGDRPYQDAPVATNPNPDREVQAEQCFOLLGDIWSNDCSLSIRDARKRDKG 120

QY 115 QYFRVERGYSY-----VRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFVNA 169

DB 121 SYFRLERGMKWSYKQNLNKTQKLSVFTVLTALTRPDILILGLTSGHSRNLTCVFPWA 180

QY 170 FEECPPEFSWGTGAALSQGTPTTSHPSVLSFTPRPDQDHTDITLCHVDFSRKGVSAQRT 229

DB 181 CKQGTTPMISWIGASVSSPG--PTTARSSVLTLPKPDQDHTSLTQVTLPGTGVTTTST 238

QY 230 VRLRVAYAPRDLVISISRDNTDPPENLRVMVQANRTVLENLGNCTSLPVLEQSLCLV 289

DB 239 VRLDVSY-----PPMNLTVTFQGDATASTALNGSSLSVLEQSLRLV 282

QY 290 CVTHSSPPARLSWTQRCQVLSPPQSPDPGVLELPRVQVEHEGFTCHARHPLGSHVLSLS 349

DB 283 CAVNSNPPARLSWTQRCQVLSPPQSPDPGVLELPRVQVEHEGFTCHARHPLGSHVLSLS 342

QY 350 LSVHYKKGLISTAPSN--GAFLGIGITALLFL--CLALIIMKILPKR 392

DB 343 LSLQNEGTGSRPVSVQVTLAAVGGAGATATAFLSFCIIIFIIVRSCKRK 390

RESULT 3

US-09-046-736-2
 Sequence 2, Application US/09046736
 Patent No. 6090582

GENERAL INFORMATION:

APPLICANT: KIKLY, KRISTINE

APPLICANT: ERICKSON-MILLER, CONNIE

TITLE OF INVENTION: Sialoadhesin Family Member-3

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia

STREET: P.O. Box 980

CITY: Valley Forge

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/046,736

FILING DATE: 24-MAR-1998

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/041,885

FILING DATE: 02-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-50019

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,574
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0552Q
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 440 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-759-628-4

Query Match 28.4%; Score 769; DB 3; Length 440;
 Best Local Similarity 36.5%; Pred. No. 4.3e-59;
 Matches 190; Conservative 73; Mismatches 163; Indels 94; Gaps 15;

QY 2 LPLLLSLGGQAMGRWIRVQESVMVPEGLCHISVPCSP--SYPRQDWTGTPAYGY 59
 DB 1 MLPLLLPLWAGALAOERFQEGPSLTVQEGLCVLPCLPTLP-----ASYVGYGY 55

QY 60 WFKAVTETTKGA--PVATNHSREVMSRGRFQGLTGPAGKNCGLVIRDAQMDQESQYF 117
 DB 56 WF-----LEGADVATNDPDEVEEETGRPHLLWDPKNCGLSIRDAARRNVAIF 109

QY 118 FRVERGSYRYNFMNDGFFLKVTALTKQPDVPIPETLEFG--QPVTVICVFNMAFEECP 175
 DB 110 FRL-KGKMKYGYTSSKIYVRVNMALTRPNISIP--GPGWPPSSNLTCSVPWVCEQGT 165

QY 176 PFSWTCALSSOGTRETSHFSVLSTPDPDHDITLCHVDPSKGYSAQRTVRLVA 235
 DB 166 PFSWMSAAPHILG--PRITQSSVLITP-AQHSNLTCTQVTFPGAGVTMBERTQLNVS 222

QY 236 YAPRDVLVISRNDTPDPENLWVMSQANRTVLENLNGTSLPVLGQSLCLVCTHSS 295
 DB 223 YAPQKVAISI-----FQNSAAFKILQNTSSLVLEGOALALLCDAGN 266

QY 296 PPARLNTQGVLSQSPQDPVLELPRVQVEHEGEFTCHARHPLGSOHVLSLSVHYK 355
 DB 267 PPAHLSWFOQSPXPNATPISNTGVLELPQVGSABEGDFTCRAQHPLGSLQISLSLVHMK 326

QY 356 K-----GLISTAFSGAFLGIGITALLFLCLALIIMKILPKRRTOTETPRPRFSRSTIL 410
 DB 327 PEGRAGVL-----GAVWASITLVLVLCVCFIP-----RVKTRKKQPOCKXT 371

QY 411 DYINVVPTAGPLAQKNQKATPNSTPLPPGAPSPESKKNQKQVQLPSPFEPKSSQA 470
 DB 372 DDVNPVWVG-----SRGHQFOFGTGVISDHPAEA 401

QY 471 PESQESQELHYATLNFPGVRPEAPSPKGTQADYAEVK 510
 DB 402 GPISDEQELHYAVLHFHKVQPOE-----PKVTDTEYSEIK 437

RESULT 6
 US-08-759-628-5
 Sequence 5, Application US/08759628
 Patent No. 6225446
 GENERAL INFORMATION:
 APPLICANT: Altman, Scott W.
 APPLICANT: Rock, Fernando L.
 APPLICANT: Bazan, J. Fernando
 APPLICANT: Kastelein, Robert A.
 TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,628
 FILING DATE: 05-DEC-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,574
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0552Q
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 421 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-759-628-5

Query Match 25.6%; Score 693.5; DB 3; Length 421;
 Best Local Similarity 43.0%; Pred. No. 1.7e-52;
 Matches 157; Conservative 53; Mismatches 132; Indels 23; Gaps 4;

QY 3 LPLLLSL--GGQAMGRWIRVQESVMVPEGLCHISVPCSPSYPRQDWTGTPAYGYWF 61
 DB 1 MPLLLPLWAGSLQEKPVYELQVQKSVTVQEGLCVLPVCSFYSPWMSWYSSPPLYYWF 60

QY 62 KAVTETTKGAPVATNHSREVMSRGRFGLTGPAGKNCGLVIRDAQMDQESQYFPERVE 121
 DB 61 RDGEPIPYAEVVAIINPDNRVKETQGRFRLDGVQKNCGLSIGDARMEETGSYFPERVE 120

QY 122 RGSYRYNFMNDGFFLKVTALTKQPDVPIPETLEFG--QPVTVICVFNMAFEECPSPFS 179
 DB 121 RGRDVXYSYQKNLNLVLTALIEKPDHLSGPLESGLWRPTRLSCSLPGSCVAGPPLTFS 180

QY 180 WTGAALSSQGTKTTSFHSVLSTPDPDHDITLCHVDPSKGYSAQRTVRLVA 239
 DB 181 WTGNAXAPMT-PRPXAPELTLTPREDHGTMLTOMKQGAQVITEXTVQLNVSTAPQ 239

QY 240 DLVTSISRDNTPOPPENLWVMSQANRTVLENLNGTSLPVLGQSLCLVCTHSSPPAR 299
 DB 240 TITIF-----RNGIALEILQNTSYLPVLEGOALRLLLCDAPSNPPAH 280

QY 300 LSWTQRCQVLSQSPQDPVLELPRVQVEHEGEFTCHARHPLGSOHVLSLSVHYKGLI 359
 DB 281 LSWFQSPALNATPISNTGILELRVRSABEGFTCRAQHPLGFLQIFLNLVSLPQLL 340

QY 360 STAPS 364
 DB 341 GPSCS 345

RESULT 7
 US-08-896-537A-3
 Sequence 3, Application US/08896537A
 Patent No. 6590088
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Gentz, Reiner L.

APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CD33-Like Protein
FILE REFERENCE: 1488.0480001
CURRENT APPLICATION NUMBER: US/08/896,537A
CURRENT FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: 60/022,481
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 364
TYPE: PRT
ORGANISM: Homo sapiens
US-08-896-537A-3

Query Match 25.6%; Score 693; DB 4; Length 364;
Best Local Similarity 33.2%; Pred. No. 1.5e-52;
Matches 170; Conservative 59; Mismatches 135; Indels 148; Gaps 10;

QY 1 MLLPLLSSLLGGSOAMDGRFWRVQESVMVPEGLCISVPCGSFSPRODWTGSTPAYGYW 60
DB 1 MPELLLLPLWAGALAMPENFLQVESVTVQEGLCVLPCTFFPIPYDKNSPVHGYW 60
QY 61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESOYFFRV 120
DB 61 FREGAIIISGDSVATNKLDQVEQETQGRFLLGSPSRNCSLSIVDARRRDNCSYFFRM 120
QY 121 ERGSYRVNFMNDGFLLKVTALTQKPDYVIPETLEPGQPVTIVCVFNWAFBECPPSPESW 180
DB 121 ERGS-TKYSYKSPQSVSHVTDUTHPKILIPGTLEPGHKNLTCVSWACQGGTPPIFSW 179
QY 181 TGAALSSQGTPTTSHFSVLSFTPPQDHTDILCHVDVFSRKGVSQAQTVRLRAYAPRD 240
DB 180 LSAAPTSLG-PRTHSSVLIITPPQDHGINLTCQVKFAGAVTTEITQINVTYVQ- 236
QY 241 LVISIRONTDPPENLRVMVSOANRTVLENGNCTSLPVLEGQSLCLVCVTHSSPPARL 300
DB 237 ----- 236
QY 301 SWTORGQVLSQSPDPGVLELPRVQVEHEGEFTCHARHPLGSHVLSLSVHYKKGLIS 360
DB 237 -----NPTGIFPG-----DGS-----GKET-----RAGLV- 258
QY 361 TAFSNGAFIGITALLFLCLALIIIMKILPKRRTOTETPRFRSHSTILYINVVPTAG 420
DB 259 ---HGAIGAGGTALLALCLIFFIVKTHRRKAARTAVGSDNTHPT----- 302
QY 421 PLAQRNQAQATNSPRTPLPGAPSPESKKNQKQYQLPSPEPKSSTQAPESQESQEL 480
DB 303 -----TGSAGPKHQKNSK-----LHGPTETSSCSGAAPTVMDEBEL 338
QY 481 HYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 512
DB 339 HYASLNFHGMNP-----SKDSTSYSEVRTQ 364

RESULT 8
US-09-046-736-4
Sequence 4, Application US/09046736
Patent No. 6030582
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rafter & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-046-736-4

Query Match 21.2%; Score 573; DB 3; Length 374;
Best Local Similarity 29.8%; Pred. No. 5.4e-42;
Matches 156; Conservative 63; Mismatches 138; Indels 166; Gaps 10;

QY 2 LLPLLSSLLGGSOAMDGR-----FWIRVQESVMVPEGLCISVPCGSFSPRODWTGSTP 55
DB 1 MLLLLLLPLWGRVERVEMQSKNDYSLTMQSSVTVQEGCVHVRCSFSYPVDSQTDSDP 60
QY 56 AYGWFKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQ 115
DB 61 VHGYWFRAGNDISWKPAPVATNPAWQVQETRDPRFLLGDFQTKNCTLSIRDARMSDAGR 120
QY 116 YFRRVGRSVRVNFMNDGFLLKVTALTQKPDYVIPETLEPGQPVTIVCVFNWAFBECPP 175
DB 121 YFRMEKGN-IKWYKIDQLSVNVTY----- 145
QY 176 PFSWTAALSSQGTPTTSHFSVLSFTPPQDHTDILCHVDVFSRKGVSQAQTVRLRVA 235
DB 146 ----- 145
QY 236 YAPRDLVISIRONTDPPENLRVMVSOANRTVLENGNCTSLPVLEGQSLCLVCVTHSS 295
DB 146 -----PQNLTVTYVQEGGTASTALGNSSLSVLEGQSLRLVCAVDN 188
QY 296 PPARLSWTRGQVLSQSPDPGVLELPRVQVEHEGEFTCHARHPLGSHVLSLSVHYK 355
DB 189 PPARLSWTRSLTYPSQSPNPLVLEL-QVHLGDEGEFTCRAQNSLGSQSHVSLNLSLQOE 247
QY 356 -----KGLISTAFSNGAFIGITALLFLCLALIIIMKILPKRRTOTETTPRFRSHS 407
DB 248 YTGKRPVSGVLL-----GAVGGAGATALVLSFCVFIWV---RSCRKKSARP----- 293
QY 408 TILDYINVVPTAGTAPLQAKRQKATNSPRTPLPGAPSPESKKNQKQYQLPSFPPEPKSS 467
DB 294 -----AADVDIGNK-----DANTIRGSASQGNLTESWADDNPRHH 329
QY 468 TQAPESQESQELHYATLNFPGVRPRPEARMKPGTQADYAEVK 510
DB 330 GLAAHSSGEEREIQYAPLSPHKGEPO-DLSGQEATNNYSEIK 371

RESULT 9
US-09-513-999C-7159
Sequence 7159, Application US/09513999C
Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.02.24
CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-26
SOFTWARE: Patent.pm
SEQ ID NO 7159
LENGTH: 64
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 28
OTHER INFORMATION: Xaa-His or Gln
US-09-513-999C-7159
Query Match 12.8%; Score 346; DB 4; Length 64;
Best Local Similarity 98.4%; Pred. No. 3.6e-23;
Matches 63; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
131 MNDGFLKVTALQKPDVPIPETLEPGQPVVICVFNWAFECPPSPSWTGAALSSQGT 190
1 MNDGFLKVTALQKPDVPIPETLEPGQPVVICVFNWAFECPPSPSWTGAALSSQGT 60
191 KPPT 194
61 KPPT 64
RESULT 10
US-09-513-999C-4599
Sequence 4599, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.02.24
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4599
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -16..-1
OTHER INFORMATION: score 11.3
OTHER INFORMATION: seq FLLLSLLGGSSQA/MD
FEATURE:
NAME/KEY: UNSURE
LOCATION: 24
OTHER INFORMATION: Xaa-Ala or Ser
US-09-513-999C-4599
Query Match 7.4%; Score 200; DB 4; Length 56;
Best Local Similarity 89.1%; Pred. No. 1.9e-10;
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
1 MLLPLLSLLGGSSQAMDGRFWIRVQESVNVPEGLCISVXLLFLP 46

Db 1 MLLPLLSLLGGSSQAMDGRFWIRVQESVNVPEGLCISVXLLFLP 46
RESULT 11
US-08-408-095-31
Sequence 31, Application US/08408095
Patent No. 5858678
GENERAL INFORMATION:
APPLICANT: Chinnadurai, Govindaswamy
TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-408-095-31
Query Match 6.6%; Score 177.5; DB 2; Length 501;
Best Local Similarity 20.0%; Pred. No. 4.3e-07;
Matches 107; Conservative 82; Mismatches 182; Indels 165; Gaps 24;
QY 25 VQESVMVPEGLCISVPCSF-----SYPRQDWTGTFPAYGYWFKAVTETTKGAPVATNHQS 79
Db 80 IQNEMPIREGDVTLSNYSNPSVTRYEW---KPHGAWEEPSLGLVKIQVWMDNTT 135
QY 80 REVEMSTRGRFOLTGDPKNCNCSLVIRDAQMDQESQYFFRVERGSYVRYNFNDGFLKV 139
Db 136 --TACARCNCSWASPVALNVQYAPRDVVR-----LSWTQRCQVLSPSQ 167
QY 140 TALTKQPDVPIPETLEPGQPVVICVFNWAFECPPSPSW--TGAALSSQGTKPPTSHF 197
Db 168 KPLSE-----IHSNYSVSLQCDPSSSHPK--EVQFPWEXNGRLG---KESQNF 212
QY 198 SVLSFTPRPDHDTLTCVDFSRKGVSAQRTVRLVAYAPROLVISISDNTDPENL 257
Db 213 DSIS---PEDAGS-YSCWYNN--IGQTASKAWTLEVLVYAPRLRVSMSPGD----- 258
QY 258 RVMSQANRTVLENLNGTSLPVLGOSLCLVCVTHSSPEAR----LSWTQRCQVLSPSQ 313
Db 259 -----QVMEKSAITLTCESDANPVSHYTWFDNNQ-----SL 291
QY 314 PSDGVLELPRVQVEHEGETCHARPLGSHQVSL--LSVHYKKGLISTAFSNGAFLGIG 372
Db 292 PHHSQKRLRFPVKVQHSQAYWCQGTNSVKGSRSPSLTLYVYSPETI-----GRVAVG 345
QY 373 ITALLFLCLALIMKI---LPKR--RTOTET-----PRPFRSHSTILDYIN 414
Db 346 LGS-----CLAILLAIICGLKLRWRKWTQSQQLQENSSQCSQFFVNVKVRAPLSEGP 401

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QY 415 VVPTAGPLAQKQKATPNSPTPLPPGAPSPESK-----KNQKQY 456
D 402 SLGCYNPMMDGISTYTLRFPENIPRTGDAESSEMQRPRCTDDTVTYSALHKQVGDY 461
QY 457 Q--LPSFPPKSTQAPESQSEBELHYATLNFPGVRPEARMKPGTQADYAEVK 510
D 462 ENVIDFPE-----DEGIHSELIQGVGERFQAQ-----ENVDIVLK 500

RESULT 12
US-09-638-649-5
; Sequence 5, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Murine
US-09-638-649-5

Query Match 6.4%; Score 172.5; DB 4; Length 403;
Best Local Similarity 23.3%; Pred.No. 8.7e-07;
Matches 101; Conservative 46; Mismatches 139; Indels 147; Gaps 21;

QY 100 NCSLVIRDAQMODESQYFRV--ERGSYVRVNFMDGFLKVTALTQKPDVYIPET--LEP 156
D 80 NGSLLLPATGIVDEGTFRCRATNRGKVKSNR-----VRVYQIPGKPEIVDPASELTA 134
QY 157 GQPTVY-ICVFENWAECEPPPSFSW--TGAALSSQGT-----PTSHSPVLS-F 202
D 135 SVFNKVGTCVSGSY---PAGTSLWHLPGKLLIPDGKTLVKEETRRHPETGLFTRSEL 191
QY 203 TPRP-QDHDITDCHVDKRGKVSQRTVRLRVAVAPRDLVISISRDNTPPPENLRVMV 261
D 192 TVIPTQGGTTFESCSFS-LGLPRRPLNT---APIQL-----RVREPGPEGIQLLV 241
QY 262 SQANRTVLENLNGNLSLFLVLEQSLCLVCVTHSSPPARLSWTQGVLSPSQSPDPGVLE 321
D 242 EPEGGI-----VAPGTVTLTCAISAQPPQVHWIKDGAPL-PLAPSP--VLL 286
QY 322 LPRVQVEHEGEPTCHARHPLGSHVLSLSVHY-----KKGLISTAFSNGA 367
D 287 LPEVGHADGTYSCVATHSPSHGQSPSPVSIIVTGTGDEGPAEGSVGESGLTLALGI 346
QY 368 FIGITALLFLCLALIMKLLPKRTQTPTRPRFRSHSTILDYINVVPTAGPLAQKN 427
D 347 LGLGLVALL-----VAILWRK 365
QY 428 QKATNSPTPLPPGAPSPESKKNQKQYQLPSPPEPKSSTOAPESQSELHYATLNF 487
D 366 Q-----PREERK-----APESQSEDEE--RAELN- 388
QY 488 PGVRPRPEARMK 500
D 389 ----QSEEAEMPE 397

RESULT 13
US-08-602-725-32
; Sequence 32, Application US/08602725
; Patent No. 5965710
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```
; GENERAL INFORMATION:
; APPLICANT: BODMER, WALTER F
; APPLICANT: DURBIN, HELGA
; APPLICANT: SNARYN, DAVID
; APPLICANT: STEWART, LORNA MD
; APPLICANT: YOUNG, SUSAN
; APPLICANT: BATES, PAUL A
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,725
; FILING DATE: 02-FEB-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/01816
; FILING DATE: 19-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9317423
; FILING DATE: 21-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 1090-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-602-725-32

Query Match 6.2%; Score 167; DB 2; Length 464;
Best Local Similarity 23.5%; Pred.No. 3.2e-06;
Matches 85; Conservative 52; Mismatches 122; Indels 102; Gaps 18;

QY 5 LLASLLGGSQAMDGRVIRVQSVVMPEGLCISVP-----CSFSYPRQDWTGSTPAY 57
D 19 LLTASLL-----TWNPTTAQLTTESMPFNVAEGKEVLLVHNLPOQ-----LF 63
QY 58 GY-WFKAVTETTKGAPVATNHQREVMSTRGRFQITGDPAGK-----NCSLIVRDAQ 109
D 64 GYSWYKG--BRVDG-----NRQIVGAIGTQATPGPANGSGRETIYPNASLLIQNT 113
QY 110 MQDSQYFEEVERGSVYRVNFMNDGFLKVTALTQKPDVYIPETLEPGQPVVICVFNWA 169
D 114 QNDTGFTLVQ-----IKSLVNE-----EATGQPHVY----- 141
QY 170 FEECPSPFSWGTGAALSSQGTKEPTTSHFSYLSFTPRPDHDTLTCHVDPSRKGVSQRT 229
D 142 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWVNNQSLPVSP-- 189
QY 230 VRLVAVAPRDL-VISISRDNTDPPENLRVMVVSQANET--VLENLNGTSLPVLE---- 282
D 190 -RLQSLNGNATLLSVTRNDTGYECEIQNPVS-ANRSDPVLNVITYGPTTISESDT 247
QY 283 ----GQSLCLVCVTHSGSPPARLSWTQGVLSQSPSDPGVLELPRVQVHEGEFTCHAR 338
```

Db 248 YRPGANLSLSVCAASNPAPQYSLWNGTFQOSTQB-----LFIPNITVWNSGSYTCHAN 302

Qy 339 H 339

Db 303 N 303

RESULT 14

Accession No. 5169835-17

Patent No. 5169835

APPLICANT: WAI-YEE, CHAN

TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APLICATIONS

NUMBER OF SEQUENCES: 48

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/390,409

FILING DATE: 07-AUG-1989

SEQ ID NO:17:

LENGTH: 321

5169835-17

Query Match 5.7%; Score 155; DB 6; Length 321;
Best Local Similarity 24.3%; Pred. No. 2.2e-05;
Matches 73; Conservative 43; Mismatches 105; Indels 80; Gaps 15;

Qy 58 GY-WFKAIVTETTKGAPVATNHQREVMSTGRFQLTGDPAGK-----NCSLVIRDAQ 109

Db 64 GYSWYKQ--ERVDGNSLIVGY-----VIGTQATPGPAYSGRETIYPNASLLIQNVT 113

Qy 110 MQDESQYFRFRV--ERGSYVRYNFMNDGFLKVTALTQKPDVYIPET--LEPGQPVTV--ICV 165

Db 114 QNDTGFTTQV-----IKGLVNE-----EATGQFHY 141

Qy 170 FECCPPPSFSWTGAALSSQTKFTTSHFSVLSFTPRPDQHDLDLCHVDPSRKGVSAQRT 229

Db 142 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTYLWVWNNQSLPVPSP--- 189

Qy 230 VRLRVAYARDL-VISIRDNTPDPENLRVMVSAQRT--VLENLNGTSLFVLE----- 282

Db 190 -RLQLSNGNRITLLSVTRNDTGYECIQNPVS--ANRSDPVTLNVYTPDPTISPSDT 247

Qy 283 ----GOSLCLVCTHSSPPARLSWQGVLSQPSQSDPGVLELPRVQVHEHGEFTCHAR 338

Db 248 YRPGANLSLSVCAASNPAPQYSLWNGTFQOSTQB-----LFIPNITVWNSGSYTCHAN 302

Qy 339 H 339

Db 303 N 303

RESULT 15

US-09-638-649-1

Sequence 1, Application US/09638649

Patent No. 6563015

GENERAL INFORMATION:

APPLICANT: Stern, David M.

APPLICANT: Schmidt, Ann Marie

APPLICANT: Yan, Shi Du

TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED

TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND

TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND

FILE REFERENCE: 05/95/62175

CURRENT APPLICATION NUMBER: US/09/638,649

CURRENT FILING DATE: 2000-08-14

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 1

LENGTH: 416

TYPE: PRT

ORGANISM: Bos Taurus

US-09-638-649-1

Query Match

Best Local Similarity 5.7%; Score 153.5; DB 4; Length 416;

Mismatches 23.5%; Pred. No. 4.2e-05;

Matches 108; Conservative 57; Mismatches 170; Indels 125; Gaps 25;

Qy 62 KAVTETTKGAPVATNHQREVMSTGRFQLTGDP-----AKGNCSLVIRDAQ 109

Db 32 KPLVLNCKGAP-KKPPQQLWKLT-GRTEAWKVLSPQDQWDSVARVLNGLSLPVG 89

Qy 110 MQDESQYFRFRV--ERGSYVRYNFMNDGFLKVTALTQKPDVYIPET--LEPGQPVTV--ICV 165

Db 90 IQDEGTFRCRATSRSGKTKSNYR-----VRVQIPGKPEIVDPASELMAGVENKVGTCV 144

Qy 166 FNWAFEECPPPPSFSW--TGAALSSQ-----TK--PTTSHF---SVLSFTPRPDQHD 210

Db 145 SEGQY---PAGTLNWLDDGKTLIPDGKGVSVKETEKRHPKTIGLTTHSELMLVTPARGG-- 199

Qy 211 TDLTCHVDFS---RKGVSAQRTVRLRVAVAPRDLVISIRDNTPDPENLRVMVSAQRT 267

Db 200 ---ALHETFCSTPG:PRRALHT---APIQLRVWSEHRGEGP--NVDAPVLKEVQL 250

Qy 268 VLENLNGTSLPVLGOSLCLVCTHSSPPARLSWQGVLSQPSQSDPG-VLELPRVQ 326

Db 251 VVEPEGGA---VAPGGTTLTCEAPAQPPQIHWIKDGRPL---PLPEGPMLLLPVVG 302

Qy 327 VEHEGEFTCHARHPLGSHVLSLSVHYK-----GLISTAFSNGAFLGIG 372

Db 303 PEDGTYSCVATHPSHGQPSRAVSVTIIETGEGTTAGSVGEGLETALT:GILGLG 362

Qy 373 ITALLFLCLALIIIMKILPKRTQTETPRPRFSRHSHTILDYINVVPTAGPLAQRNOKATP 432

Db 363 TVALL-----IGVIVHRRRQ-----RKQBRKVP 387

Qy 433 NSPRTPLPPGAPSPESKKNQKQYQLPSFPE-PKSSTQAP 471

Db 388 E-----NQEERAEELNQPEPEAEBSSTGGP 416

Search completed: November 5, 2004, 13:58:21

Job time : 19.3484 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 14.2346 Seconds
(without alignments)
3460.797 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLLPILLSLLGSGQAMDGR.....RPEARMPKGTQADYAEVKFQ 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:**

1: Pirl:**

2: pirl2:**

3: pirl3:**

4: pirl4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	694	25.6	364	2	A30521		myeloid cell surfa
2	528	19.5	403	2	I52590		m33-B isoform - mo
3	304.5	11.3	626	1	A61084		myelin-associated
4	302.5	11.2	620	2	JH0593		Schwann cell myeli
5	295.5	10.9	626	1	BNRT3		myelin-associated
6	289.5	10.7	582	1	BNRT3S		myelin-associated
7	288.5	10.7	637	2	B3785		myelin-associated
8	245	9.1	1694	2	S50065		sialoadhesin - mou
9	227	8.4	862	2	I49583		differentiation an
10	220.5	8.1	868	2	A46512		CD22 homolog/B lym
11	206.5	7.6	647	2	A35648		B-cell adhesion pr
12	202.5	7.5	847	2	JH0371		B-cell adhesion pr
13	186	6.9	526	1	A32164		biliary glycoprote
14	184	6.8	402	2	T03062		probable advanced
15	180	6.7	4391	2	A30896		perlecan precursor
16	167	6.2	321	2	JH0395		biliary glycoprote
17	167	6.2	351	2	JH0396		biliary glycoprote
18	167	6.2	417	2	JH0394		biliary glycoprote
19	167	6.2	464	2	C30127		transmembrane carc
20	156.5	5.8	336	2	C27658		pregnancy-specific
21	155	5.7	3707	2	S18252		heparan sulfate pr
22	153.5	5.7	416	1	A42879		advanced glycosyla
23	151.5	5.6	1241	2	T37190		nephrit - human
24	149	5.5	210	2	JC4122		pregnancy-specific
25	149	5.5	538	2	JC2457		vascular cell adhe
26	148.5	5.5	5175	2	T20992		hypothetical prote
27	148.5	5.5	5198	2	T43290		hemocentin precurs
28	147.5	5.5	1906	1	S68235		myosin-light-chain
29	147	5.4	332	2	JN0067		pregnancy-specific

30 144.5 5.3 26926 1 I38344
31 143 5.3 702 2 A36319
32 142.5 5.3 1232 2 T43027
33 141.5 5.2 739 2 JN0581
34 141 5.2 402 2 A54312
35 140.5 5.2 392 1 RWHUPD
36 140.5 5.2 417 1 RWHUPA
37 140.5 5.2 428 2 I57486
38 140.5 5.2 428 2 S30032
39 140 5.2 521 2 S34338
40 140 5.2 628 2 J38000
41 139.5 5.2 419 2 J4123
42 139 5.1 404 1 I61596
43 138.5 5.1 349 2 A34815
44 138.5 5.1 495 2 A55181
45 138 5.1 324 2 G43354

ALIGNMENTS

RESULT 1

A30521

myeloid cell surface antigen CD33 precursor - human

C:Species: Homo sapiens (man)

C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004

C:Accession: A30521

R:Simmons, D.; Seed, B.

J. Immunol. 141, 2797-2800, 1988

A>Title: Isolation of a cDNA encoding CD33, a differentiation antigen of myeloid progenit

A:Reference number: A30521; MUID:89009814; PMID:3139786

A:Accession: A30521

A:Molecule type: mRNA

A:Residues: 1-364 <SIM>

A:Cross-references: UNIPROT:P20138

C:Genetics:

A:Gene: GDB:CD33

A:Cross-references: GDB:119762; OMIM:159590

A:Map position: 19q13.3-19q13.4

C:Keywords: glycoprotein; surface antigen; transmembrane protein

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-259/Domain: extracellular #status predicted <EXT>

F:260-282/Domain: transmembrane #status predicted <TM>

F:283-364/Domain: intracellular #status predicted <CYT>

F:100,113,160,209,230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.6%; Score 694; DB 2; Length 364;
Best Local Similarity 32.8%; Pred. No. 1e-39;
Matches 168; Conservative 59; Mismatches 137; Indels 148; Gaps 8;

QY 1 MLLPILLSLLGSGQAMDGRFWIRVQBSVMVPEGLCLISVFCSPSYPRQDWTGTGTPAYGYW 60

Db 1 MLLPILLSLLGSGQAMDGRFWIRVQBSVMVPEGLCLISVFCSPSYPRQDWTGTGTPAYGYW 60

QY 61 FKAVTETTKAPVATNHQSRVEMSTGRFQLTGDPKAGNCSLVIRDAQMDQESQYFPRV 120

Db 61 FKAVTETTKAPVATNHQSRVEMSTGRFQLTGDPKAGNCSLVIRDAQMDQESQYFPRV 120

QY 61 FREGAIISSGSPVATNKLQDEVEETQGRFLLGDPSPNNCSLIVDARRDNGSYFPRM 120

Db 61 FREGAIISSGSPVATNKLQDEVEETQGRFLLGDPSPNNCSLIVDARRDNGSYFPRM 120

QY 121 ERGSYVYRNFMDGFFLLKVTALTQKPDVYIPETLEPQQPVTVICVFNWAFEECPSPFSW 180

Db 121 ERGSYVYRNFMDGFFLLKVTALTQKPDVYIPETLEPQQPVTVICVFNWAFEECPSPFSW 180

QY 121 ERGSYVYRNFMDGFFLLKVTALTQKPDVYIPETLEPQQPVTVICVFNWAFEECPSPFSW 180

Db 121 ERGSYVYRNFMDGFFLLKVTALTQKPDVYIPETLEPQQPVTVICVFNWAFEECPSPFSW 180

QY 181 TGAALSSQGTPTTSHFSLVSFTPRQDHTDLTCHVDPSRKGVSQAORTVRLRVAYAPRD 240

Db 181 TGAALSSQGTPTTSHFSLVSFTPRQDHTDLTCHVDPSRKGVSQAORTVRLRVAYAPRD 240

QY 180 LSAAPTSLG--PRTHSSVLIITPRQDHTGNTLCQVKFAGVTTERTITQLNVTYYPQN 237

Db 180 LSAAPTSLG--PRTHSSVLIITPRQDHTGNTLCQVKFAGVTTERTITQLNVTYYPQN 237

QY 241 LVISISRDNTDPPENLRVMVMSQANRTVLENLNGTSLPVLGQSLVCVTHSSPPARL 300

Db 241 LVISISRDNTDPPENLRVMVMSQANRTVLENLNGTSLPVLGQSLVCVTHSSPPARL 300

QY 238 PTTGCIFF-----GDG----- 247

Db 238 PTTGCIFF-----GDG----- 247

QY 301 SWTORGQVLSPSQSDPGVLELPRVQVEHEGEFTCHARHPLGSHVLSLSVHYKGLIS 360

Db 301 SWTORGQVLSPSQSDPGVLELPRVQVEHEGEFTCHARHPLGSHVLSLSVHYKGLIS 360

QY 248 -----SKQETRAGV----- 258

Db 248 -----SKQETRAGV----- 258

```
QY 361 TAFSNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRPFSRHSSTILDYINVVPTAG 420
DB 259 ---HGAIGAGVTALLALCLLFIIVKTHRKAARTAVGNDTH-----PTTG 304
QY 421 PLAQRNKATPNSPTPLPPGAPSPESKKNQKQVLQSFPEPKSSTOAPSPQSQBEL 480
DB 305 SASPKHQKSKLRGP-----TETSSCSGAATVEMDEEL 338
QY 481 HYATLNPFGVRRPEARMKPGTQADYAEVKFQ 512
DB 339 HYASLAFHGNP-----SKDTSTSEVVRTQ 364

RESULT 2
152590
153-B isoform - mouse
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I52590
R:McMillan, E.Z.; Beverley, P.C.; Young, B.D.; Watt, S.M.
A:Title: Molecular cloning of two isoforms of the murine homolog of the myeloid CD33 ant
A:Reference number: I52590; MUID:94250900; PMID:8193354
A:Accession: I52590
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-403 <RES>
A:Cross-references: GB:S71345; NID:G551352; PIDN:AAB30842.1; PID:G551353

Query Match 19.5%; Score 528; DB 2; Length 403;
Best Local Similarity 42.2%; Pred. No. 21e-28;
Matches 122; Conservative 34; Mismatches 105; Indels 28; Gaps 4;

QY 1 MLPLLLSSLLGSSQAMDRFWIRVOESVWVPEGLICISVPCSFSPRODWTGSTPAYGVW 60
DB 1 MLPLPLFLLCAGSLAQDLFQLVAPESVTVESGLCHVPCSVFYFYSIKLT-LGPVTGSW 59
QY 61 FRVATTETKAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQVFRV 120
DB 60 LRKGVSLHSDPVATSDPQLVQKATQGRFOLLGDPKDCSLFIRDAQKNTGMVFRV 119
QY 121 ERGSYVRYNFMDGFFLKVTALTQKPDVPIPELEPGQPVTVICVFENWAFECPPPSFSW 180
DB 120 VREPFVRYKYSQSLSHVTSLSRTPDIIPTGLEAGYPSNLTCSPVWACEQGTPTFSW 179
QY 181 TGAALSSQGTKPTTSHFSLVSTFPRQDHTDITLCHVDPSRKGVSQRTVRLRVAYAPD 240
DB 180 MSTALTSLSRTTDS--SVLTFTFPQDAGTKLTCLVTFSGAGVTVERTIQI----- 229
QY 241 LVISISRDNPDPENLRVWVSQANRTVLENLGNGLTSLPVLGQSCLV 289
DB 230 -----NVRKSGQRELVLVAGSATVKLLIG--LCIV 261

RESULT 3
A61084
myelin-associated glycoprotein precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: A61084; A33263; FC2011
R:Spagnol, G.; Williams, M.; Srinivasan, J.; Golier, J.; Bauer, D.; Lebo, R.V.; Latov, N.
J. Neurosci. Res. 24, 137-142, 1989
A:Title: Molecular cloning of human myelin-associated glycoprotein.
A:Reference number: A61084; MUID:90064604; PMID:2479762
A:Accession: A61084
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-626 <SPA>
A:Cross-references: UNIPROT:P20916
R:Sato, S.; Fujita, N.; Kurihara, T.; Kuwano, R.; Sakimura, K.; Takahashi, Y.; Miyatake,
Biochem. Biophys. Res. Commun. 163, 1473-1480, 1989
A:Title: cDNA cloning and amino acid sequence for human myelin-associated glycoprotein.
```

```
A:Reference number: A33263; MUID:89392063; PMID:2476987
A:Accession: A33263
A:Molecule type: mRNA
A:Residues: 1-613; 'T', 615-626 <SAT>
A:Cross-references: GB:M29273; NID:g187292; PIDN:AAA59545.1; PID:g307156
R:Burger, D.; Pidoux, I.; Streck, A.J.
Biochem. Biophys. Res. Commun. 197, 457-464, 1993
A:Title: Identification of the glycosylated sequences of human myelin-associated glycoprotein.
A:Reference number: FC2011; MUID:94092116; PMID:7505568
A:Accession: FC2011
A:Molecule type: protein
A:Residues: 84-98 'X', 100-110; 210-222 'X', 224; 245 'X', 247-253; 309-318 'XXX'; 396-405 'X'
C:Comment: This protein is a neural cell adhesion molecule.
C:Genetics:
A:Gene: GDB:MAG; GMA
A:Cross-references: GDB:120702; OMIM:159460
A:Map position: 19q13.1-19q13.1
C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C:Keywords: brain; cell adhesion; glycoprotein; phosphoprotein; transmembrane protein
F:1-13/Domain: signal sequence #status predicted <SIG>
F:20-626/Product: myelin-associated glycoprotein #status predicted <MAT>
F:35-102/Domain: immunoglobulin homology <IMM>
F:118-120/Region: cell attachment (R-G-D) motif
F:514-536/Domain: transmembrane #status predicted <TM>
F:99,223,246,315,406,450,454/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:106/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:132/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:543,607/Binding site: phosphate (Ser) (covalent) #status predicted
F:573/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 11.3%; Score 304.5; DB 1; Length 626;
Best Local Similarity 21.1%; Pred. No. 4.9e-13;
Matches 137; Conservative 90; Mismatches 229; Indels 193; Gaps 23;

QY 21 FWIRVQ-----ESWVPEGLICISVPCSFSPRODWTGSTPAYGVWKAIVTT 68
DB 10 FWIMISASRQGHGAWMPSSISAFEGTCVSPICRDFEP--DELRPVAVHGVWVNSPYPK 67
QY 69 KGAPVATNHOSREVMETRGRFQLTGDPKAGNCSLVIRDAQMDQESQVFRVRSVRY 128
DB 68 NYPVVKERTQVHVSFQGRSLGLDLGRNCTLLSNVSPELGKYYFRGLGGYNQY 127
QY 129 NPMNDGFLKVTALTQKPDVPIPELEPGQPVTVICVFENWAFECPP--PSFSWTG--- 182
DB 128 TFSBH---SVLDTVNTPIWVPEVAVAGTEVESCVP--DNCPELRPELSMGLHEGL 180
QY 183 ---AALSS-QGTKPTTSHFSLVSTFPRQDHTDITLCHVDPSRKGVSQRTVRLRVAYAP 238
DB 181 GEPVGLGRDEGTWQVQLLHFVPTREANGHRLGCAQSFNTTLOFEGYASMDVYKPP 240
QY 239 RDLVISI-----RDNTDP-----PENLRVW----- 261
DB 241 VIVEMSGSVEAIEGSHVSLGADSNPPLLITWMDCTVLRVAEASLLELEBEVTPAED 300
QY 262 -----SQANRTV-----LENLGNGLTSLPVLGQSCLVCTVTHSSPRLSW 302
DB 301 GYVACLAENAYGQDNRTVGLSVYAPKPTVNGTMVAV--EGEIVSILCSTQSNDDPILTI 359
QY 303 TQRCQLLSPSPQSPDGVLELPRVQVEHEGEFTCHARPLGSHQVSLSLVHYKXGLI--- 359
DB 360 FKEQQLSTVIYSELQLELPAVSPEDDGEVWCVAENQVQGRATAPNLSVEFAPVLLLES 419
QY 360 -----STAF-----SNGAFL-----GIGITALLFLCLA 382
DB 420 HCAAARDTVQCLVWKNPSPFSAFELPSRNVTVNESEREFVYSERGLVITSLTTL--- 476
QY 383 LIIMKILPKRRTQETP-----RPRFSRHSSTILDY-----INVPTAGLA--- 423
DB 477 -----RGQAQAPRVICTARNLYGAKSLELPFGAHLRMWAKIGPVGAVVAFIL 526
QY 424 -----QKNQKATNSPRTPLPP-----GAPSP-ESKKNQKQYQLPSF 461
DB 527 IALVCYITQTRKKNVTSFSGAGNDPPVLFSSDFRISGAPEKYESERRLGL 586
```


A:Gene: MAG
 A:Map position: 7
 C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
 C:Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; transmembrane
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-626/Product: myelin-associated glycoprotein, long splice form #status predicted <MA>
 F:205-102/Domain: immunoglobulin homology <IMM1>
 F:318-120/Region: cell attachment (R-G-D) motif
 F:318-120/Domain: immunoglobulin homology <IMM2>
 F:340-307/Domain: immunoglobulin homology <IMM3>
 F:340-307/Domain: immunoglobulin homology <IMM4>
 F:425-490/Domain: immunoglobulin homology <IMM5>
 F:514-536/Domain: transmembrane #status predicted <TM>
 F:537-626/Domain: intracellular #status predicted <INT>
 F:99,223,246,315,332,406,450,454/Binding site: carbohydrate (Asn) (covalent) #status pre
 Query Match 10.9%; Score 295.5; DB 1; Length 626;
 Best Local Similarity 22.2%; Pred. No. 28-12;
 Matches 142; Conservative 85; Mismatches 239; Indels 173; Gaps 25;
 21 FWIRVQ-----ESVMVPEGLCISVPCSFYPRQDWTGSPAYGYWFKAVTEIT 68
 10 FWIMISASRGHWGAMWPSISAFECTVSIICRFDPF--DELPAVVGWVYFNSPYPK 67
 69 KGAPVATNHOSREVMSTRGRFOLTGDPAKGNCSLVIRDAQMDQESQYFFRVERGSYVY 128
 68 NYPPVVKSRQTVVHESFQGRSRLLDGLRLNCTLLSLTSLPELGKYYFRGLGGYNOY 127
 129 NFNWDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECP--PSFSWTGAALS 186
 128 TFSEH-----SVLDIINTPIVWPEVAVTEVSCWVP--DNCPELRPELSWLGHEGL 180
 187 SQGT-----KPTTSHFSVLSTPRPQDHTDLTCHVDFSRKGSQAQTVRLRVAYAP 238
 181 GEPTVLGRLEDEGTWVQVSLHFVPTREANGHRLGCQAAPFNTTLQFEGYASLDVKYPP 240
 239 RDLVISIS-----RDNTDP-----PENLRV-----259
 241 VIVEMNSSVEAIEGSHVSLCGADSNPPLLTWMDGMVLRVAESLYLDLEVTPEAD 300
 260 -----MVSQANRTV-----LENLNGTSLPVLEGQSLCIVCVTHSSPPARLSW 302
 301 GIYACLAENAYGQDNRTVELSVWVAPWKPTVNGTVVAV--EGETVSLCSTQSNPDILT 359
 303 TORQGVLSFQSPDQGVLELPRVQVEHEGFTCHAPHLGSGHVSLSLVHYKGLISTA 362
 360 FKEKQILATVIVESQLELPAVTPEDDGEYWCVAENQYQRATAPNLSVEFAPITLES 419
 363 FSNAGFLGIGITALLFLCLALI-----IMKILPKRR--TQETPRP-RFSRHSITLDVI 413
 420 HCAAADTV-----QCLCVKSNPEPSVAPELFSRVTVVNETEREFFVYSRGLL-LT 471
 414 NVVPTAGP-----LAQKRNQKATNSRTEL-----PPGA-----443
 472 SILTLRGAQAPPRVICTSRNLYGT--QSLLEPFGAHLRLWAKIGPVGAFAFILAIV 530
 444 ---PSPESSKKNQKQVQLPSF-----PEKSSQCAPESESQS-----478
 531 CYITQTRRRKNVTES---PSFAGDNPHVLYSPERFIS--GAPDKYSEKRLGSRRLGL 586
 479 -----ELHYATLNFEGVRPRPEAMPKGTQADYAEVK 510
 507 RGPPELDLSYSHSDL-GKRPTKDSYTLTBEAEYAEIR 624
 RESULT 6
 BNR13
 myelin-associated glycoprotein precursor, short splice form - rat
 N:Alternate names: 18236; brain neuron cytoplasmic protein 3; MAG
 C:Species: Rattus norvegicus (Norway rat)
 Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text_change 16-Jun-2000
 C:Accession: B29028; B27185; A60055
 R:Lai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.

Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
 A:Title: Two forms of 18236/myelin-associated glycoprotein, a cell adhesion molecule for
 A:Reference numbers: A29028; MUID:87232001; PMID:2438699
 A:Accession: B29028
 A:Molecule type: mRNA
 A:Residues: 1-582 <LAI>
 A:Cross-references: GB:M22357; NID:g205271; PIDN:AAA41558.1; PID:g205272
 R:Salzer, J.L.; Holmes, W.P.; Colman, D.R.
 J. Cell Biol. 104, 957-965, 1987
 A:Title: The amino acid sequences of the myelin-associated glycoproteins: homology to the
 A:Reference number: A27185; MUID:8716195; PMID:2435742
 A:Accession: B27185
 A:Molecule type: mRNA
 A:Residues: 419-582 <SAL>
 A:Cross-references: GB:X06554; NID:g56614; PIDN:CAA29797.1; PID:g1334302
 R:Tropak, M.B.; Johnson, P.W.; Dunn, R.J.; Roder, J.C.
 Brain Res. Mol. Brain Res. 4, 143-155, 1988
 A:Title: Differential splicing of MAG transcripts during CNS and PNS development.
 A:Reference number: A60055
 A:Accession: A60055
 A:Molecule type: mRNA
 A:Residues: 565-582 <TRO>
 C:Comment: The sequence contains five presumably extracellular domains that are distantly
 C:Comment: The short form is found in the adult; the long form predominates in early post
 C:Genetics:
 A:Gene: MAG
 A:Map position: 7
 C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
 C:Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; transmembrane
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-582/Product: myelin-associated glycoprotein, short splice form #status predicted <M>
 F:315-102/Domain: immunoglobulin homology <IMM1>
 F:315-102/Region: cell attachment (R-G-D) motif
 F:315-102/Domain: immunoglobulin homology <IMM2>
 F:315-102/Domain: immunoglobulin homology <IMM3>
 F:340-307/Domain: immunoglobulin homology <IMM4>
 F:425-490/Domain: immunoglobulin homology <IMM5>
 F:514-536/Domain: transmembrane #status predicted <TM>
 F:537-582/Domain: intracellular #status predicted <INT>
 F:99,223,246,315,332,406,450,454/Binding site: carbohydrate (Asn) (covalent) #status pre
 Query Match 10.7%; Score 289.5; DB 1; Length 582;
 Best Local Similarity 23.2%; Pred. No. 4.6e-12;
 Matches 110; Conservative 64; Mismatches 185; Indels 115; Gaps 14;
 21 FWIRVQ-----ESVMVPEGLCISVPCSFYPRQDWTGSPAYGYWFKAVTEIT 68
 10 FWIMISASRGHWGAMWPSISAFECTVSIICRFDPF--DELPAVVGWVYFNSPYPK 67
 69 KGAPVATNHOSREVMSTRGRFOLTGDPAKGNCSLVIRDAQMDQESQYFFRVERGSYVY 128
 68 NYPPVVKSRQTVVHESFQGRSRLLDGLRLNCTLLSLTSLPELGKYYFRGLGGYNOY 127
 129 NFNWDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECP--PSFSWTGAALS 186
 128 TFSEH-----SVLDIINTPIVWPEVAVTEVSCWVP--DNCPELRPELSWLGHEGL 180
 187 SQGT-----KPTTSHFSVLSTPRPQDHTDLTCHVDFSRKGSQAQTVRLRVAYAP 238
 181 GEPTVLGRLEDEGTWVQVSLHFVPTREANGHRLGCQAAPFNTTLQFEGYASLDVKYPP 240
 239 RDLVISIS-----RDNTDP-----PENLRV-----259
 241 VIVEMNSSVEAIEGSHVSLCGADSNPPLLTWMDGMVLRVAESLYLDLEVTPEAD 300
 260 -----MVSQANRTV-----LENLNGTSLPVLEGQSLCIVCVTHSSPPARLSW 302
 301 GIYACLAENAYGQDNRTVELSVWVAPWKPTVNGTVVAV--EGETVSLCSTQSNPDILT 359
 303 TORQGVLSFQSPDQGVLELPRVQVEHEGFTCHAPHLGSGHVSLSLVHYKGLISTA 362
 360 FKEKQILATVIVESQLELPAVTPEDDGEYWCVAENQYQRATAPNLSVEFAP 413


```
QY 242 --VISISRDNDPPP-----ENLRVMSQA-----NRTVLNL 272
: : : : :
Db 345 GNSVSLQCDFSSSHPEKQVFEKNGRLLGKESQLNFDISPEDAGSYSCWVWNSIGQTA 404
: : : : :
QY 273 GNGTSLPVL-----EGSLCLVCVTHSSPPAR-----LSWTQRCQVLSLP 311
: : : : :
Db 405 SKAWTLEVLVAPRRLRVNSPGDQWEGKSATLTCESDANPVSHYTFWFDWNNQ-----458
: : : : :
QY 312 SOPSPPGVLELPRVQVEHEGEFTCHARHPLGSHQVLSLSVSHYKKGLISTAFSNGAFLG 370
: : : : :
Db 459 SLPYHSQKLRLFPVKVQHSYGAWCQGTNSVGKRSPLSLTLTVYISPEITL-----GRRVA 512
: : : : :
QY 371 IGITALLFLCLALIMKI-----LPRK--RTQETPRPRSRHSTILDTINVVPTAGPLAQ 424
: : : : :
Db 513 VGLGS-----CLAILLILAICGLQLRWKRTQSQOGLQENS-----SGQFF 554
: : : : :
QY 425 KENQKATPNSPTPLPPGAPSPESKKNQKQVLPSPFPBKSGSTQAPSQBSQBSLHYAT 484
: : : : :
Db 555 VRNKKVR-----RAPLSEG-----PHSLGCV-----NPMWEDGISYTT 587
: : : : :
QY 485 LNPFGVRPRPEARMKGTQADYAEVK 510
: : : : :
Db 588 LRF-----PEMNIPRTGDAESSEMQ 607
: : : : :

RESULT 12
JB0371
B-cell adhesion protein CD22 beta splice form precursor - human
N:Alternate names: B-cell membrane protein CD22
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0371; 156171
R:Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
J. Exp. Med. 173, 137-146, 1991
A:Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell interaction
A:Reference number: JH0371; MUID:91086838; PMID:1985119
A:Accession: JH0371
A:Molecule type: mRNA
A:Residues: 1-847 <WIL>
A:Cross-references: UNIPROT:O60926; GB:X59350; NID:G36090; PIDN:CAA42006.1; PID:G36091
A:Experimental source: B lymphocyte
A>Note: the authors translated the codon AAT for residue 358 as Met
R:Wilson, G.L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.
J. Immunol. 150, 5013-5024, 1993
A:Title: Genomic structure and chromosomal mapping of the human CD22 gene.
A:Reference number: 156171; MUID:93267103; PMID:8496502
A:Accession: 156171
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 121-269, 'T', 271-473, 'K', 475-614, 'R', 616-638, 'Y', 640-711, 777-847 <WIL2>
A:Cross-references: GB:S61375; NID:G385980; PIDN:AAC18956.1; PID:G3184492
C:Genetics:
A:Gene: GDB:CD22
A:Cross-references: GDB:127545; OMIM:107266
A:Map position: 19q13.1-19q13.1
A:Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-847/Product: B lymphocyte cell adhesion protein #status predicted <MAT>
F:346-398/Domain: immunoglobulin homology <IM1>
F:609-661/Domain: immunoglobulin homology <IM2>
F:688-706/Domain: transmembrane #status predicted <TRA>
F:67,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (covalent)
F:764,789/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.5%; Score 202.5; DB 2; Length 847;
Best Local Similarity 21.0%; Pred. No. 5.7e-06;
Matches 98; Conservative 69; Mismatches 182; Indels 117; Gaps 19;

QY 1 MLPLLLLSLLGGSQAMDCRFWT-RVQESVMVPEGLCISVPCFS-----YPRQ 48
: : : : :
Db 3 LLGPWLLLVLEVLAFSDSSKWFEPETLIYAWEGACVWIPCTYRALDGLDLSFILFHPN 62
: : : : :
```

```
QY 49 DWTGSTPAYWFKAVTETTKGAPVATNHOSREVEMSTRGRFOLTGDPAKGNCSLVIRDA 108
: : : : :
Db 63 EYKNNTSKFD--GTRLYESTKDGKVP-----SEQKRVQFLGDKNK-NCTLSHPV 109
: : : : :
QY 109 QMDESQYFRVRBERGSVRYNFMNDGFFLKVTALTOKPDDVYIPETLEPGOPVTVICVFN- 167
: : : : :
Db 110 HMDSGQLGRMES-----KTEKMERIHNVSRPPPHIQLPEIQESQEVTLTCLLNF 165
: : : : :
QY 168 -----WAFEECPPPSFWTGAALSQGTPTTSHFSVLSPFPRPDHDTDLTCHV 217
: : : : :
Db 166 SCGYPIQLQWLLGVBMRQAAVTSTSL-----TIKSVFTSELKFSQWSHHGKIVTCOL 221
: : : : :
QY 218 -DFSRKGVN-----AORTVRLRVAYAPRLVLI-----SISRDNTPPPE--- 255
: : : : :
Db 222 QDADGKFLSNDTVQLNVKHTPKLEIKVTPSDAIVREGDSVTWTCVSSSN-----PEYTV 277
: : : : :
QY 256 -----NLR-VMVSOQNR---TVLENLNGTGS----- 277
: : : : :
Db 278 SWLKDGTSLLKQNTFTLNLREVTKDQSGKYCCQVNDVGPGRSEEVFLQVYAPEPSTVQ 337
: : : : :
QY 278 ---LPVLEGSQLCLVCVTHSSP-PARLSWTQRCQVLSFSPQSPGVLELPRVQVEHEGEF 333
: : : : :
Db 338 ILHSPAVEGSGVFLCLMSLANPLFTNTVYHNGKEM---QGRTEEKVHIPIKLDPWHAGTY 394
: : : : :
QY 334 TCHARHPLGS--QHVSLSLSVHYKKGLISTAFSNGAFLGIGITALL 377
: : : : :
Db 395 SCVAENILGTGQCGAELDVQYPPKVTIVIQNPPIREGDVTVL 440
: : : : :

RESULT 13
A32164
biliary glycoprotein 1 precursor, splice form a - human
N:Alternate names: transmembrane carcinoembryonic antigen 1 (TMI-CEA); transmembrane carcinoembryonic antigen 1
C:Species: Homo sapiens (man)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: A32164; A30127; B30127; A48078; S45664; S655939; A30847; G44476
R:Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta, I.
Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
A:Reference number: A32164
A:Contents: erratum
A:Accession: A32164
A:Molecule type: mRNA
A:Residues: 1-526 <HIN>
A:Cross-references: UNIPROT:P13688; GB:J03858; NID:G179439; PIDN:AAA51826.1; PID:G179440
R:Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta, I.
Proc. Natl. Acad. Sci. U.S.A. 85, 6953-6963, 1988
A:Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of biliary glycoprotein I
A:Reference number: A94206; MUID:88320555; PMID:2457922
A:Contents: annotation
A>Note: the sequence shown in this reference has been completely corrected in reference 1
R:Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; Ke J. Cell Biol. 108, 267-276, 1989
A:Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs
A:Reference number: A92752; MUID:89139550; PMID:2537311
A:Accession: A30127
A:Molecule type: mRNA
A:Residues: 1-526 <BAR1>
A:Cross-references: EMBL:X16354; NID:G37197; PIDN:CAA34404.1; PID:G37198; EMBL:X14784
A:Experimental source: splice form a
A:Accession: B30127
A:Molecule type: mRNA
A:Residues: 1-319, 'D', 417-526 <BAR2>
A:Cross-references: EMBL:X14831; NID:G37199; PIDN:CAA32940.1; PID:G37200; EMBL:X14784
A:Experimental source: splice form b
R:Barnett, T.R.; Drake, L.; Pickle II, W.
Mol. Cell. Biol. 13, 1273-1282, 1993
A:Title: Human biliary glycoprotein gene: characterization of a family of novel alternative splicing variants
A:Reference number: A48078; MUID:93140765; PMID:8423792
A:Accession: A48078
A:Molecule type: mRNA
A:Residues: 124-141, 'H', 417-526 <BAR3>
A:Cross-references: GB:M76742; NID:G179480; PIDN:AAA57142.1; PID:G179481
```

Experimental source: splice form x

Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBI:123606)

Note: neither the complete nucleic acid sequence nor the complete translation are shown

W. H. J. Biochem. 223, 529-541, 1994

Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene family

Accession: S45664

Accession: S45664

Status: preliminary

Molecule type: DNA

Residues: 1-21 <HAU>

Cross-references: EMBL: X67277; NID: g29447; PIDN: CAA47694.1; PID: g606777

W. H. J. Biochem. 231, 104-114, 1995

Title: Characterization and transcriptional activity of the mouse biliary glycoprotein

Accession: S65939

Accession: S65939

Status: preliminary; translation not shown

Molecule type: DNA

Residues: 1-21 <NED>

Cross-references: EMBL: X67277; NID: g29447; PIDN: CAA47694.1; PID: g606777

Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992

Note: only a part of the coding sequence is given

Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.

Genomics 14, 384-390, 1992

Title: Identification of three new genes and estimation of the size of the carcinoembryonic

Accession: A44476; MUID: 93052339; PMID: 1427854

Contents: annotation; alignment of related sequences

Genetics:

Gene: GDB: BGP

Cross-references: GDB: 127992; OMIM: 109770

Map Position: 19q13.2

Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal

Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein

F:1-136/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F:1-34/Domain: signal sequence #status predicted <SIG>

F:35-526/Product: biliary glycoprotein 1, splice form a #status predicted <WATA>

F:35-428/Domain: extracellular #status predicted <EXT>

F:35-319, '417-526/Product: biliary glycoprotein 1, splice form b #status predicted <M>

F:35-319, '417-526/Product: biliary glycoprotein 1, splice form x #status predicted <M>

F:160-217/Domain: immunoglobulin homology <IMM1>

F:252-301/Domain: immunoglobulin homology <IMM2>

F:341-398/Domain: immunoglobulin homology <IMM3>

F:425-454/Domain: transmembrane #status predicted <TM>

F:453-526/Domain: intracellular #status predicted <INT>

F:104, 111, 115, 152, 182, 197, 208, 224, 232, 254, 274, 288, 292, 302, 309, 345, 351, 363, 378, 405, 475/B1

Query Match 6.9%; Score 186; DB 1; Length 526;

Best Local Similarity 21.5%; Pred. No. 4.2e-05;

Matches 130; Conservative 80; Mismatches 200; Indels 196; Gaps 31;

QY 5 LLLSLGSGQMDGFWVQVSVVPEGLCISVP-----CSFSYPRQDWTGSTAY 57

DB 19 LUTASLL-----TFWAPPTTAQTTFSPMPVAGKEVLLVHNUPOQ-----LF 63

QY 58 GY-WPKAVTETTKGAPVAINHOSREVMSTGRFQLTGDPAKG-----NCSLVIRDAQ 109

DB 64 GYSWYKG-ERVDG-----NRQIVGVAIGTQATPGPANSGRETIYVNASLLIQNVT 113

QY 110 MQDESQYFRVERGVSRYVNFMDGFLKVTALTQKPDVYIPETLEPQPVTVICFNWA 169

DB 114 QNDTGYTYIQV-----IKSLVNE-----EATQGHVY----- 141

QY 170 FEECPSPSWTGAALSSQGTPTTSHFVLGFTPRPDQDHTDLTCHVDSEKGVSAQRT 229

DB 142 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWVNNQSLPSP--- 189

QY 230 VRLRVAYAPDL-VISISRDNTDPDENLRVMSQANFT--VLENLNGTSLFVLE----- 282

DB 190 -RLQNGNRTLTLLSVTNDTGPVECEIQNPVS-ANRSDPVTLVNTVGPDTFTTSPSDT 247

QY 283 ----GQSLCLVCTHSSPPARLSWTORGQVLSQPSDPSGVLELPRVQVHEGFTCHAR 338

DB 248 YVRGANLSVCAASNPAPQYVWMLNGTFOOSTOE-----LPFNPITVNNSGSYTCHEAN 302

QY 339 HPL-GSQHVSLSLVHYKKGLISTAFS-----NCAFLIGITALLFLCLA 382

DB 303 NSVTGCKNTTV-----KTIIVTSLSPVAKPOIKASKTIVTGDKDSVNL-----CST 350

QY 383 L---IIMKILPKRRTQTETPRPFSRHSHTILDYINVP-----TAGP 421

DB 351 NDTGISIRWFFKQSLSPSEEMKLSQGNLTLS-INPVKREDAGTYWCEVFNPISKNSDP 409

QY 422 LAQKRNQVATNSPRTPLPPCA-----PPESKKN 451

DB 410 IMLNVYNALEFQ--ENGLSPGAIAGIVGVVVALVALVALACTLHFPGKTRASDQDRLT 467

QY 452 QKKQVQLPSPFPEPKSSTQ--APESQESQELHYATLNFPGVVRP-RPEARMPK--GTQADY 506

DB 468 EHK-----PSVSNHTQDHSNDPPNKXNEVYSLNFEAQQTPTQSASPSLTATEIY 520

QY 507 AEVKPQ 512

DB 521 SEVKKQ 526

RESULT 14

T09062

probable advanced glycosylation end-products receptor precursor - mouse

N:Alternate names: RAGE

C:Species: Mus musculus (house mouse)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09062

R:Rosen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Loretz, C.; Sci

submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region

A:Reference number: Z16543

A:Accession: T09062

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-402 <ROW>

A:Cross-references: UNIPROT: O35444; EMBL: AF030001; NID: g2564945; PID: g2564950

C:Genetics:

A:Gene: RAGE

A:Map position: 17

A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2

C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology

C:Keywords: receptor; transmembrane protein

F:31-100/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 184; DB 2; Length 402;

Best Local Similarity 23.4%; Pred. No. 4.1e-05;

Matches 101; Conservative 46; Mismatches 139; Indels 146; Gaps 20;

QY 100 NCSLVIRDAQMQDESQYFRV--ERGSYRYNFMNDGFLKVTALTQKPDVYIPET-LEP 156

DB 80 NGSLLPATGIVDEGTFRCATNRKGEKVSRYR-----VRVYQIPGKPEIVDPASLTA 134

QY 157 GQPVTV-ICVFNWAFECPPPSFSW--TGAALSQGTGK-----PTTSFVSLS-F 202

DB 135 SVPNKVTCTVSEGSY---PAGTILSHLDGKLLIPDGKETLVKEETRRHPETGLTLRSEL 191

QY 203 TPRPDHDTLTCHVDSEKGVSAQRTVRLRVAYAPDLVISISRDNTDPDENLRVMS 262

DB 192 TVIPTQGTHTFTSCFS-LGLPFRRLPLNT---AFIQL-----RVREPGPPGIGLLVE 241

QY 263 QANRTVLENLNGTSLPVLEGQSLCLVCTHSSPPARLSWTORGQVLSQPSDPSGVLEL 322

DB 242 PEGGI-----VAPGGTVITLCAISAGPPQVHWIKDKAPL-PLASP- -VLLL 286

QY 323 PRVQVEHEGFTCHARPLGSHQVLSLSVHY-----KKGLISTAFNGAF 368

DB 287 PEVGEDEGTYSVATPHSGPQESPPVSTRVTETGDEGPAEGSVGESGLTALALGIL 346

QY 369 LGICITALLFLCLALLIMKILPKRRTQTETPRPFSRHSHTILDYINVPVTAGPLACKNQ 428

Db 347 GGLGVALL-----VCAILLRKEQ 365

QY 429 KATPNSPTLPFGAPSPKXNQKQVQLPSFPKXSTQAPESQSEELHYATLNP 488

Db 366 -----PRREERK-----APESQSEEE--RAELN-- 387

QY 489 GVRPRPEARMKP 500

Db 388 -----QSEEAEMPE 396

RESULT 15

A38096

N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote

C;Species: Homo sapiens (man)

C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 12-Jul-2004

C;Accession: A38096; S19256; S79946; A41059; A40306; B33625; A41736

R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.

J. Biol. Chem. 267, 8544-8557, 1992

A;Title: Primary structure of the human heparan sulfate proteoglycan from basement membr

tor, laminin, neural cell adhesion molecules, and epidermal growth factor.

A;Reference number: A38096; MUID:92235084; PMID:1569102

A;Accession: A38096

A;Molecule type: mRNA

A;Residues: 1-4391 <MUR>

A;Cross-references: UNIPROT:P98160; GB:M85289; NID:G184426; PIDN:AAA52700.1; PID:G184427

R;Kallunki, P.; Tryggvason, K.

J. Cell Biol. 116, 559-571, 1992

A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD pro

cell adhesion molecules, and epidermal growth factor.

A;Reference number: A41736; MUID:92112994; PMID:1730768

A;Accession: S19256

A;Molecule type: mRNA

A;Residues: 1-57, 'D', 59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R',

71-2979, 'H', 2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-3

A;Cross-references: EMBL:X62515; NID:G29469; PIDN:CAA4373.1; PID:G29470

R;Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.

Genomics 11, 389-396, 1991

A;Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the g

A;Reference number: A41059; MUID:92120660; PMID:1685141

A;Accession: A41059

A;Molecule type: mRNA

A;Residues: 1-57, 'D', 59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R',

71-2979, 'H', 2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-4

A;Cross-references: EMBL:X62515; NID:G29469; PIDN:CAA4373.1; PID:G29470

R;Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.

Genomics 10, 673-680, 1991

A;Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellula

A;Reference number: A40306; MUID:91365376; PMID:1679749

A;Accession: A40306

A;Molecule type: mRNA

A;Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 <DOD>

A;Cross-references: GB:M64283; NID:G184424; PIDN:AAA52699.1; PID:G184425

R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van der

J. Cell Biol. 105, 3199-3211, 1989

A;Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal

anes.

A;Reference number: A33625; MUID:90078352; PMID:2687294

A;Accession: B33625

A;Molecule type: protein

A;Residues: 1379-1384, 'X', 1386-1398, 'X', 1390-1398 <HE2>

A;Accession: A33625

A;Molecule type: protein

A;Residues: 2166-2171, 'X', 2173-2175, 'X', 2177-2185 <HE3>

A;Note: peptide potentially matches four different regions of sequence shown

C;Genetics:

A;Gene: GDB:HSPG2

A;Cross-references: GDB:126372; OMIM:142461

A;Map position: lp36.1-1p36.1

C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembrar

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-4391/Product: perlecan #status predicted <MAT>

F;22-193/Domain: I <DOM1>

F;194-530/Domain: II <DOM2>

F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F;531-1676/Domain: III <DOM3>

F;1159-1206/Domain: laminin-type EGF-like homology <LEG>

F;1553-1610/Domain: laminin-type EGF-like homology <EG7>

F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>

F;1677-3686/Domain: IV <DOM4>

F;2007-2034/Domain: transmembrane #status predicted <TRM>

F;3687-4391/Domain: V <DOM5>

F;3845-3880/Domain: EGF homology <EGF1>

F;3888-3921/Domain: EGF homology <EGF>

F;3993-4106/Domain: laminin G repeat homology <LG2>

F;4147-4175/Domain: EGF homology <EGF2>

F;4149-4151/Region: motor neuron attachment (L-R-E) motif

F;4299-4301/Region: motor neuron attachment (L-R-E) motif

F;65.71.76/Binding site: heparan sulfate (Ser) (covalent) #status predicted

F;89.554.1755.2121.3072.3105.3279.3780.3836.4068/Binding site: carbohydrate (Asn) (coval

F;2995.9333.4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 6.7%; Score 180; DB 2; Length 4391;

Best Local Similarity 20.4%; Pred. No. 0.0015;

Matches 129; Conservative 68; Mismatches 214; Indels 222; Gaps 30;

QY 18 DGRWIRVOESVMVPEGLICTSVPCSFSPQRD--WT--GSTPA-----XYW----- 60

Db 3119 EGPVWVKGVATLE--CVSA-----GEPRSSARWTRISSTPAKLEQRTVGLMDSHAVLQ 3171

QY 61 -----FKAVTETTKGAPVATNHQSRVEMSTRG----- 88

Db 3172 ISSAKPSDAGTYVCLQAALGTAQKQVEVIVDTGMAFGAPQVQAEELTVEAGHTATL 3231

QY 89 RFQITGTPA-----KGNCSLVIRDAQWDESOYFFRVERGVSRYNF 130

Db 3232 RCGATGSPAPTHWKSRLSPWQHRLEGDTLLIPRVAQ-QDSQYI-----CNA 3280

QY 131 MNDGFFLKVTAL--TQKPD--VIYPE--TLEFGQVTVICVFNWAFECPPPSFSGTAA 184

Db 3281 TSPAGHAEATILIHVESPPYATTVEHASVQAGETVOLQCLAHGT---PDLTFQWSRVG 3336

QY 195 LSSQGTRETTSHFSVLSTFPQPDHDLCHVDLCHVDFSKVSAQRTVLRVAYAPRDL-VI 243

Db 3337 SSLFGR--ATARNELLHFERAAPDSGRYCRV--TNKVGSAEAFQALLVQGPFGSLPAT 3392

QY 244 SISRDNTPPPENLRVMVQSANRVLENLNGTSLPVL-----QSLCLVCTVTHSSPPAR 299

Db 3393 SIPAGSTP-----TVQVT-----POLETKSIGASVEFFHCAPVSDQGTQ 3430

QY 300 LSWTQRCQVLSPSPQSPGVLELPRVQVEHEGETCHARPLGSHQVLSLSLVHYKGLI 359

Db 3431 LRWFKEGQLPFGHSDGVGLRIQNLQSCQGTYICQAHGFWGKAQASQALVIOALEPSVL 3490

QY 360 STAFSNGAFLGIGITALLFLCLALLIMKILPKRTQTETPRFS----- 404

Db 3491 INIRTSVQTVVVG--HAVEFECLAL-----GDPKQVTKVKGHLRPGIVQS 3536

QY 405 -----RHSTILD-----YINVVPTAGP-----LAQKRNQKATFNSRTP----- 438

Db 3537 GGVVRIAHVELADAGQKCTATNAAGTTQSHVLLLVQALPOISMPEQVVRVPAAGAAVPPC 3596

QY 439 LPFGAPSPESKKNQKQVQLPSFPKXSTQAPESQSEELHYATLNPFGVRP----- 493

Db 3597 IASGYPTPDISWS-KLDGSLP-----PDSR-----LENNMLPSVRPQDAGTY 3639

Ox 494 -----PEARMPKGTQADYA 507
|| : || :
Db 3640 VCTATNRQGVKAFALQVPERVVVYFTQTPYS 3672

Search completed: November 5, 2004, 13:51:01
Job time : 18.2346 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 59.6073 Seconds
(without alignments)
3081.324 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLPLLLSLGGSQAMDGR.....RPEARMPKGTQDYAEVKFQ 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2706	100.0	512	3 AAY97542	Aay97542 Human obe
2	2580.5	95.4	697	5 AAU87087	Aau87087 Sialic ac
3	2576.5	95.2	697	6 ADA27153	Ada27153 Human nov
4	2576.5	95.2	697	7 ADJ26582	Adj26582 Siglec-10
5	2576.5	95.2	697	8 ADI37010	Adi37010 Novel hum
6	2576.5	95.2	697	8 ADL82805	Adl82805 Human PRO
7	2417	89.3	710	7 ADD19314	Add19314 Human sec
8	2278	84.2	544	5 AAU87074	Aau87074 Sialic ac
9	2265	83.7	544	2 AAY41724	Aay41724 Human PRO
10	2265	83.7	544	3 AAB44280	Aab44280 Human PRO
11	2265	83.7	544	6 AAU29082	Aau29082 Human PRO
12	2265	83.7	544	6 ABUS8438	Abus8438 Human PRO
13	2265	83.7	544	6 ABUS8006	Abus8006 Novel hum
14	2265	83.7	544	6 ABUS4321	Abus4321 Human sec
15	2265	83.7	544	6 ABR66195	Abr66195 Human sec
16	2265	83.7	544	6 ABR65585	Abr65585 Human sec
17	2265	83.7	544	6 ABUS9525	Abus9525 Human sec
18	2265	83.7	544	6 ABUS2764	Abus2764 Human PRO
19	2265	83.7	544	6 ABUS9885	Abus9885 Novel hum
20	2265	83.7	544	6 ABR68134	Abr68134 Human sec
21	2265	83.7	544	6 ABUS96187	Abus96187 Novel hum
22	2265	83.7	544	6 ABUS2618	Abus2618 Human sec
23	2265	83.7	544	6 ABO08695	Abo08695 Human sec
24	2265	83.7	544	6 ABO02747	Abo02747 Human sec
25	2265	83.7	544	6 ABR74901	Abr74901 Human sec

ALIGNMENTS

RESULT 1
AAY97542
ID AAY97542 standard; protein; 512 AA.

XX AC AAY97542;

DT 12-FEB-2001 (first entry)

DE Human obesity protein binding protein-2 homologue #1.

KW Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
obesity-related disorder; therapy.

OS Homo sapiens.

XX WO200059942-A2.

PD 12-OCT-2000.

PF 22-MAR-2000; 2000WO-US006682.

PR 02-APR-1999; 99US-0127667P.

XX (ELIL) LILLY & CO ELI.

XX Su EW, Wei J;

DR WPI: 2000-664992/64.

DR N-FSDB; AAA37847.

XX New human obesity protein binding protein-2 homologue nucleic acids,
polynucleotides and polypeptides useful for producing medicament for
treating obesity and/or obesity-related disorders.

PS Claim 9; Page 86-88; 92pp; English.

XX This sequence is a human obesity protein binding protein-2 homologue (hOB
-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may
be used for the manufacture of a medicament for the treatment of obesity
and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful
as probes or amplification primers in the detection, quantification or
isolation of gene sequences or transcripts, for recombinant expression of
hOB-BP2h polypeptides, as immunogens in the preparation and screening of
antibodies, and in sense or antisense suppression of one or more hOB-BP2h
genes or nucleic acids, host cell or tissue in vivo or in vitro.
CC Antigenic epitope-bearing peptides and polypeptides are useful for
raising or screening antibodies that specifically binds to the hOB-BP2h
polypeptides

Abu94563 Human sec
Abo25226 Novel hum
Abu85636 Human PRO
Abu98796 Novel hum
Abu98011 Novel hum
Abu91717 Novel hum
Abu72232 Novel hum
Abu89410 Human PRO
Abu86251 Human sec
Abu67464 Human sec
Abu80492 Human PRO
Abu99410 Human sec
Abr9800 Human sec
Abo16323 Human sec
Abr92223 Human sec
Abo18864 Human sec
Abr78285 Human sec
Abu85021 Novel hum
Abo00160 Novel hum
Abo11492 Human sec

26 2265 83.7 544 6 ABR94563
27 2265 83.7 544 6 ABO25226
28 2265 83.7 544 6 ABUS5636
29 2265 83.7 544 6 ABUS98796
30 2265 83.7 544 6 ABUS98011
31 2265 83.7 544 6 ABUS91717
32 2265 83.7 544 6 ABUS72232
33 2265 83.7 544 6 ABUS89410
34 2265 83.7 544 6 ABUS86251
35 2265 83.7 544 6 ABUS67464
36 2265 83.7 544 6 ABUS80492
37 2265 83.7 544 6 ABUS99410
38 2265 83.7 544 6 ABR9800
39 2265 83.7 544 6 ABO16323
40 2265 83.7 544 6 ABR92223
41 2265 83.7 544 6 ABO18864
42 2265 83.7 544 6 ABR78285
43 2265 83.7 544 6 ABUS5021
44 2265 83.7 544 6 ABO00160
45 2265 83.7 544 6 ABO11492

```

XX      Sequence 512 AA;
30      Query Match
30      Best Local Similarity 100.0%; Score 2706; DB 3; Length 512;
30      Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      1 MLLPLLSSLLGGQAMDGFWIRVQESVMVPEGLCISVPCSFSPYRQDWTGSTPAYGW 60
XX      1 MLLPLLSSLLGGQAMDGFWIRVQESVMVPEGLCISVPCSFSPYRQDWTGSTPAYGW 60
XX      61 FKAVTETTKGAPVATNHQSRVEMSTGRFQLTGDPKAGNCSLVIRDAQVQDSQYFFRV 120
XX      61 FKAVTETTKGAPVATNHQSRVEMSTGRFQLTGDPKAGNCSLVIRDAQVQDSQYFFRV 120
XX      121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFECPPPSFSW 180
XX      121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFECPPPSFSW 180
XX      181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
XX      181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
XX      241 LVISISRDNTPDPEENLRVMVQANRTVLENLNGTSLPVLEGQSLCLVCTHSSPPARL 300
XX      241 LVISISRDNTPDPEENLRVMVQANRTVLENLNGTSLPVLEGQSLCLVCTHSSPPARL 300
XX      301 SWTQRCQVLSQPSQSDPGVLELPRVQVHEGFTCHAPLQSGHVSLSVHYKKGLIS 360
XX      301 SWTQRCQVLSQPSQSDPGVLELPRVQVHEGFTCHAPLQSGHVSLSVHYKKGLIS 360
XX      361 TAFNSGAFLGIGITALLFLCLALIIKKILPKRRTQTETPRPFSRHSSTILDYINVVPTAG 420
XX      361 TAFNSGAFLGIGITALLFLCLALIIKKILPKRRTQTETPRPFSRHSSTILDYINVVPTAG 420
XX      421 PLAQRNCKATPNSPTLPPGAPSPESKKNQKQYQLPSFPKPSSTQAPESQSOEEL 480
XX      421 PLAQRNCKATPNSPTLPPGAPSPESKKNQKQYQLPSFPKPSSTQAPESQSOEEL 480
XX      481 HYATLNPFGVRPRPEARMKGTQADYAEVKFQ 512
XX      481 HYATLNPFGVRPRPEARMKGTQADYAEVKFQ 512
XX      RESULT 2
XX      ID AAU87087 standard; protein; 697 AA.
XX      AC AAU87087;
XX      DT 05-JUN-2002 (first entry)
XX      DE Sialic acid-binding Ig-related lectin, Siglec-BMS-I3-995-3.
XX      KW Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
XX      KW immune system disease; leukaemia; allergy; inflammatory disease;
XX      KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
XX      KW psoriasis; rheumatoid arthritis; conjunctivitis.
XX      OS Homo sapiens.
XX      OS Synthetic.
XX      PN W020208257-A2.
XX      PD 31-JAN-2002.
XX      PF 20-JUL-2001; 2001MO-US023082.
XX      PR 21-JUL-2000; 2000US-0220139P.
XX      PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX      PI Longphre M, Chang H, Whitney G;

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XX      WPI: 2002-241565/29.
XX      N-PSDB; ABK43373.
XX      Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
XX      molecules useful for treating immune system diseases such as asthma,
XX      PT leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
XX      Example 11: Fig 6; 209pp; English.
XX      The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
XX      related lectin) protein (I). Pharmaceutical compositions comprising (I)
XX      are useful for treating immune system diseases such as asthma, leukaemia
XX      or other allergic or inflammatory diseases. Extracellular domains of (I)
XX      represent potential markers for screening, diagnosis, prognosis, follow-
XX      up assays, and imaging methods. (I) is useful as a target for drugs which
XX      inhibit inflammation, tissue damage and remodeling in asthma, and
XX      inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
XX      disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
XX      also useful for monitoring the course of disease or disorders, and for
XX      identifying agents that bind with and/or modulate the biological activity
XX      of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
XX      useful in diagnosis and/or prognosis methods, and to detect the presence
XX      and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS
XX      proteins in a biological sample. (II) are useful as nucleic acid probes
XX      are useful for screening genomic library to isolate a genomic clone of
XX      SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
XX      diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
XX      The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
XX      expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
XX      AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
XX      invention
XX      SQ Sequence 697 AA;
XX      Query Match 95.4%; Score 2580.5; DB 5; Length 697;
XX      Best Local Similarity 73.2%; Pred. No. 3.6e-195;
XX      Matches 510; Conservative 1; Mismatches 1; Indels 185; Gaps 2;
XX      1 MLLPLLSSLLGGQAMDGFWIRVQESVMVPEGLCISVPCSFSPYRQDWTGSTPAYGW 60
XX      1 MLLPLLSSLLGGQAMDGFWIRVQESVMVPEGLCISVPCSFSPYRQDWTGSTPAYGW 60
XX      61 FKAVTETTKGAPVATNHQSRVEMSTGRFQLTGDPKAGNCSLVIRDAQVQDSQYFFRV 120
XX      61 FKAVTETTKGAPVATNHQSRVEMSTGRFQLTGDPKAGNCSLVIRDAQVQDSQYFFRV 120
XX      121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFECPPPSFSW 180
XX      121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFECPPPSFSW 180
XX      181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
XX      181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
XX      241 LVISISRDNTPD----- 252
XX      241 LVISISRDNTPDPEQGNVPYLEAQKQFLRLCAADSQPPATLSMWLQNRVLSSSH 300
XX      253 -----PPENLRVMVQANRTVLE 270
XX      301 WGRPLGLLPGVKAGDSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVQANRTVLE 360
XX      271 NLNGTSLPVLEGQSLCLVCTHSSPPARLSWTORGQVLSQPSQSDPGVLELPRVQVEHE 330
XX      361 NLNGTSLPVLEGQSLCLVCTHSSPPARLSWTORGQVLSQPSQSDPGVLELPRVQVEHE 420
XX      331 GEFTCHARHPLGSHQVLSLSVHY----- 354
XX      421 GEFTCHARHPLGSHQVLSLSVHYSPKLLGSPCSWEAEGJHCSCSSQASPAPSLRWMLGE 480
XX      355 -----K 355

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Db 481 ELLEGNSQDSFEVTPSSAGPWANSLSLHGGLSSGLRLRCBANVHGAQSGSILQLPDK 540
Qy 356 KGLISTAFNGAFGLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 415
Db 541 KGLISTAFNGAFGLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 600
Qy 416 VPTAGLAQRNCKATPNSRPTPLPGAPSPSKNKKYQLPSPPEPKSSTQAPESOE 475
Db 601 VPTAGLAQRNCKATPNSRPTPLPGAPSPSKNKKYQLPSPPEPKSSTQAPESOE 660
Qy 476 SOBELHYATLNFPGVPRPEARMKCTQADYAEVKFQ 512
Db 661 SOBELHYATLNFPGVPRPEARMKCTQADYAEVKFQ 697

RESULT 3
ADA27153
ID ADA27153 standard; protein; 697 AA.
XX
AC ADA27153;
DT
XX 20-NOV-2003 (first entry)
XX Human novel secreted protein from cDNA HDPCL05 #2.
XX
KW cytostatic; antiinflammatory; immunomodulator; neuroprotective;
KW hemostatic; gene therapy; cancer; inflammation; immune disorder;
KW neurological disorder; blood clotting disorder; food additive;
KW preservative; human; secreted protein.
XX
OS Homo sapiens.
XX
XX US2003055231-A1.
XX
XX 20-MAR-2003.
XX
XX 29-OCT-2001; 2001US-00984130.
XX
XX 28-OCT-1998; 98US-0105971P.
XX 27-OCT-1999; 99MO-US025031.
XX 19-APR-2000; 2000US-0198407P.
XX 30-OCT-2000; 2000US-0243792P.
XX 18-APR-2001; 2001US-00836353.
XX
XX (NIJU/) NI J.
XX (YOUN/) YOUNG P E.
XX (KENN/) KENNY J J.
XX (OLSE/) OLSEN H S.
XX (MOOR/) MOORE P A.
XX (WEIY/) WEI Y.
XX (GREE/) GREENE J M.
XX (RUBE/) RUBEN S M.
XX (LIUD/) LIU D.
XX (CROC/) CROCKER P R.
XX
XX Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
PI Ruben SM, Liu D, Crocker PR;
XX
XX WPI; 2003-567103/53.
XX N-PSDB; ADA27152.
XX
XX New human secreted nucleic acid molecules and polypeptides, useful for
PT preventing, treating, or ameliorating a medical condition, such as
PT cancer, inflammation, immune disorders, neurological and blood clotting
PT disorders.
XX
XX Claim 11; Page 383-385; 454pp; English.
XX
XX The invention relates to an isolated nucleic molecule that is at least
XX 98% identical to 18 human cDNA sequences representing 12 novel genes
CC encoding secreted proteins or a polynucleotide fragment of the cDNA
CC sequence contained in American Type Culture Collection (ATCC) deposit No.
CC defined in the specification, its species homologue, a variant or allelic

CC variant of the polynucleotide having a polynucleotide capable of
CC hybridising under conditions the polynucleotide, where the polynucleotide
CC does not hybridise under stringent conditions to a nucleic acid molecule
CC having a nucleotide sequence of only A or T residues. Also included are
CC recombinant vectors, host cells (for producing the polypeptide), the
CC secreted polypeptide (comprising a sequence that is at least 95%
CC identical to a polypeptide fragment, domain, epitope, full-length
CC protein, variant, allelic variant or species homologue), antibodies that
CC specifically bind to the polypeptides, diagnosing, treating, preventing
CC or ameliorating a medical condition by administering the polynucleotide
CC or the polypeptide, the gene corresponding to the cDNA sequence and
CC identifying an activity in a biological assay (by expressing the cDNA
CC sequence in a cell, isolating the supernatant, and detecting an activity
CC in a biological assay and identifying the protein in the supernatant
CC having the activity). The polypeptides, nucleic acids and antibodies are
CC useful for diagnosing a pathological condition or a susceptibility to a
CC pathological condition, such as cancer, inflammation and other immune
CC disorders, neurological and blood clotting disorders (many examples are
CC given in the specification). The nucleic acids are also useful for
CC chromosome identification, radiation hybrid mapping or long-range
CC restriction mapping. The polypeptides and antibodies are useful for
CC providing immunological probes for differential identification of the
CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
CC agonist or antagonist may also be used as a food additive or preservative
CC to increase or decrease storage capabilities, fat content or other
CC nutritional components. The present is a secreted protein of the
CC invention.
XX
SQ Sequence 697 AA;
Query Match 95.2%; Score 2576.5; DB 6; Length 697;
Best Local Similarity 73.0%; Pred. No. 7.4e-195;
Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;
Qy 1 MLLPLLSSLLGGQAMDRFWIRVQESVMVPEGLICISVPCSFYSPQDWTGSTPAYGYW 60
Db 1 MLLPLLSSLLGGQAMDRFWIRVQESVMVPEGLICISVPCSFYSPQDWTGSTPAYGYW 60
Qy 61 FKAVTETTKGAPVATNHQSRVEMSTRGRFOLTGDPKAGNCSLVIRDAQMDESOYFPRV 120
Db 61 FKAVTETTKGAPVATNHQSRVEMSTRGRFOLTGDPKAGNCSLVIRDAQMDESOYFPRV 120
Qy 121 ERGSYRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQVTVICVFNWAFEECPSPFSW 180
Db 121 ERGSYRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQVTVICVFNWAFEECPSPFSW 180
Qy 181 TGAALSSQGTPTTSHFSVLSTFTPRPDHDTLTCVDFSRKGVSAORTVRLRAYAPRD 240
Db 181 TGAALSSQGTPTTSHFSVLSTFTPRPDHDTLTCVDFSRKGVSAORTVRLRAYAPRD 240
Qy 241 LVISISRDNTPD----- 252
Db 241 LVISISRDNTALBPQGNVPYLEAKQGFRLRLCAADSPATLSWLNQNRVLSSHP 300
Qy 253 -----PENLRVMVSOANRTVLE 270
Db 301 WGRPLGLEFSGVXAGDSGRYTCRAENRLGQQRALDLSVOYPPENLRVMVSOANRTVLE 360
Qy 271 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTORGVLSPSQSDPGVLELPRVQVEHE 330
Db 361 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTORGVLSPSQSDPGVLELPRVQVEHE 420
Qy 331 GEFTCHARHPLGSHVLSLSLVHY----- 354
Db 421 GEFTCHARHPLGSHVLSLSLVHYSPKLLGLPSCSWEAEGLHCSCSSQASPAPSLRWLGE 480
Qy 355 -----K 355
Db 481 ELLEGNSQDSFEVTPSSAGPWANSLSLHGGLSSGLRLRCBANVHGAQSGSILQLPDK 540
Qy 356 KGLISTAFNGAFGLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 415

541 KGLISTAFSNGAFGLIGITALLFLCLALIMKILPKRRTQTETPRFRSHSTILDYINV 600
 416 VPTAGPLAQRNKAATNSRPTLPPCAPSPESKKNQKQYQLPSPFPKSSSTQAPESQE 475
 601 VPTAGPLAQRNKAATNSRPTLPPCAPSPESKKNQKQYQLPSPFPKSSSTQAPESQE 660
 476 SQEELHYATLNFQVRPRPBARPKGTQADYAEVKFQ 512
 661 SQEELHYATLNFQVRPRPBARPKGTQADYAEVKFQ 697

RESULT 4

ADD26582

ID ADD26582 standard; protein; 697 AA.

XX AC ADD26582;

XX 15-JAN-2004 (first entry)

XX Siglec-10 amino acid sequence SEQ ID NO:7.

XX human; cell surface protein; immunoglobulin; BGS-19; cytostatic;
 XX gynaecological; immunosuppressive; antiinflammatory; antiasthmatic;
 XX antidiabetic; dermatological; gene therapy.

XX Homo sapiens.

XX W02003083078-A2.

XX 09-OCT-2003.

XX 28-MAR-2003; 2003WO-US009676.

XX 28-MAR-2002; 2002US-0368422P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Lee LM, Feder JN, Siemers NQ, Wu S, Chen J;

XX WPI; 2003-804052/75.

XX New isolated nucleic acid molecule encoding BGS-19 polypeptides, useful
 XX for preventing, treating or ameliorating a medical condition, such as a
 XX disorder related to aberrant immunoglobulin cell surface receptor
 XX activity.

XX Example 1; SEQ ID NO 7; 224pp; English.

XX The present invention describes human cell surface protein with
 XX immunoglobulin folds, designated BGS-19 (I). (I) has cytostatic,
 XX gynaecological, immunosuppressive, antiinflammatory, antiasthmatic,
 XX antidiabetic and dermatological activities, and can be used in gene
 XX therapy. (I) can be used for preventing, treating or ameliorating a
 XX medical condition, such as a disorder related to aberrant immunoglobulin
 XX cell surface receptor activity; a cellular adhesion disorder; a disorder
 XX related to hyper- or hypo-immunoglobulin receptor activity; a disorder
 XX related to aberrant signal transduction; a reproductive disorder; a
 XX female reproductive disorder; an ovarian disorder; ovarian cancer;
 XX dysfunctional uterine bleeding; amenorrhoea; primary gynaecorrhoea;
 XX sexual dysfunction; infertility; pelvic inflammatory disease;
 XX endometriosis; placental aromatase deficiency; premature menopause;
 XX placental dysfunction; hormone deficiency; oestrogen deficiency; aberrant
 XX androgen metabolism; aberrant onset of female puberty; aberrant showing
 XX of female primary sexual characteristics; aberrant showing of female
 XX secondary sexual characteristics; precocious puberty; precocious
 XX pseudopuberty; incomplete isosexual precocity; premature thelarche;
 XX premature adrenarche; premature pubarche; polycystic ovarian disease;
 XX aberrant ovarian cycle; menorrhagia; metrorrhagia; menometrorrhagia;
 XX dysmenorrhoea; hypomenorrhoea; polymenorrhoea; dysfunctional uterine
 XX bleeding; resistant-ovary syndrome; hermaphroditism; immune disorders;
 XX inflammatory disorders; arthritis; asthma; immunodeficiency diseases such
 XX as AIDS; leukaemia; rheumatoid arthritis; granulomatous disease;
 XX inflammatory bowel disease; sepsis; acne; neutropenia; neutrophilia;

CC psoriasis; hypersensitivities; such as T-cell mediated cytotoxicity;
 CC immune reactions to transplanted organs and tissues; such as host-versus-
 CC graft and graft-versus-host diseases; or autoimmune disorders;
 CC autoimmune infertility; Addison's Disease; haemolytic anaemia;
 CC antiphospholipid syndrome; rheumatoid arthritis; dermatitis; allergic
 CC encephalomyelitis; glomerulonephritis; Goodpasture's Syndrome; Graves'
 CC Disease; Multiple Sclerosis; Myasthenia gravis; Neuritis; Ophthalmia;
 CC Bullous Pemphigoid; Pemphigus; Polyendocrinopathies; Purpura; Reiter's
 CC Disease; Stiff-Man Syndrome; autoimmune thyroiditis; Systemic Lupus
 CC Erythematosus; Autoimmune Pulmonary Inflammation; Guillain-Barre Syndrome
 CC ; insulin dependent diabetes mellitus; autoimmune inflammatory eye
 CC disease; lens tissue injury; demyelination; systemic lupus erythematosus;
 CC drug induced haemolytic anaemia; rheumatoid arthritis; Sjogren's disease;
 CC and scleroderma. The present sequence is given in comparison with BGS-19
 CC in the present invention.

XX SQ Sequence 697 AA;

XX Query Match 95.2%; Score 2576.5; DB 7; Length 697;

XX Best Local Similarity 73.0%; Pred. No. 7.4e-195;

XX Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;

QY 1 MLLPLLSSLLGGSQAMDGRFWIRVQSVVMVPEGLCLISVPCSPSYPRQDMTGSTPAYGYW 60

DB 1 MLLPLLSSLLGGSQAMDGRFWIRVQSVVMVPEGLCLISVPCSPSYPRQDMTGSTPAYGYW 60

QY 61 FKAVTTTKGAPVATNHQSVREVMSTRGRFQLTGDPKAGMCSLVIRDAQMDESQYFVRV 120

DB 61 FKAVTTTKGAPVATNHQSVREVMSTRGRFQLTGDPKAGMCSLVIRDAQMDESQYFVRV 120

QY 121 ERGSYRYNFMNDGFELKVITALTKQPDVYIPETLEPGQVTVICVFNWAECECPSPFSW 180

DB 121 ERGSYRYNFMNDGFELKVITALTKQPDVYIPETLEPGQVTVICVFNWAECECPSPFSW 180

QY 181 TGAALSSQGTKPTTSHFVSLSFTPRPDQDHTDLTCHVDTSRKGVSQRTVRLRVAYAPRD 240

DB 181 TGAALSSQGTKPTTSHFVSLSFTPRPDQDHTDLTCHVDTSRKGVSQRTVRLRVAYAPRD 240

QY 241 LVISISRDNTPD-----252

DB 241 LVISISRDNTPALEFPQGNVPLYEAQKQFLRLCAADSQPPATLSWLVQNRVLSSSH 300

QY 253 -----PPENLRVMVSOANRTVLE 270

DB 301 WGPRLGLELPVYKAGDSGRVTCRAENRLGSGQALDLSVQYPPENLRVMVSOANRTVLE 360

QY 271 NLNGTSLPVLEGQSLCLVCTHSSPPARLSWTQRGQVLSQSDPGVLELPRVQVEHE 330

DB 361 NLNGTSLPVLEGQSLCLVCTHSSPPARLSWTQRGQVLSQSDPGVLELPRVQVEHE 420

QY 331 GEFTCHARHPLGSGHVSLSLVHY-----354

DB 421 GEFTCHARHPLGSGHVSLSLVHYSPKLLGSPCSWBAEGLHCSCSSQASAPSLRWLGE 480

QY 355 -----K 355

DB 481 ELLEGSSQDSFEVTPSSAGPWANSLSLRGLSSGLRLRCEAMNVHGAQSGSLQLPDK 540

QY 356 KGLISTAFSNGAFGLIGITALLFLCLALIMKILPKRRTQTETPRFRSHSTILDYINV 415

DB 541 KGLISTAFSNGAFGLIGITALLFLCLALIMKILPKRRTQTETPRFRSHSTILDYINV 600

QY 416 VPTAGPLAQRNKAATNSRPTLPPCAPSPESKKNQKQYQLPSPFPKSSSTQAPESQE 475

DB 601 VPTAGPLAQRNKAATNSRPTLPPCAPSPESKKNQKQYQLPSPFPKSSSTQAPESQE 660

QY 476 SQEELHYATLNFQVRPRPBARPKGTQADYAEVKFQ 512

DB 661 SQEELHYATLNFQVRPRPBARPKGTQADYAEVKFQ 697

RESULT 5
 ADI37010

ID ADI37010 standard; protein; 697 AA.
XX
AC ADI37010;
XX
DI 22-APR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO 71236.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor; receptor;
KW differentiation factor; neurotrophic factor; hormone; cell receptor;
KW receptor-ligand interaction; cytoskeletal; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
PN WO2004004649-A2.
XX
PD 15-JAN-2004.
XX
PF 08-JUL-2003; 2003WO-US021083.
XX
PR 08-JUL-2002; 2002US-0394485P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld J, Wood W, Wu T;
XX
DR WPI; 2004-142912/14.
DR N-PSDB; ADI37009.
XX
PS Claim 10; SEQ ID NO 10; 118pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neurotrophic factors and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is the amino acid sequence of a human PRO protein of the
CC invention.
XX
SQ Sequence 697 AA;
Query Match 95.2%; Score 2576.5; DB 8; Length 697;
Best Local Similarity 73.0%; Pred. No. 7.4e-195;
Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;
QY 1 MLLPLLLSLLGGSQMDGRFIRVOESVYVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
DB 1 MLLPLLLSLLGGSQMDGRFIRVOESVYVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATHQREVENMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
DB 61 FKAVTETTKGAPVATHQREVENMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
QY 121 ERGSYVRYNFMNDGFFLVKVTALTKQEDVVIPELPGQPVVICVFNWAFESCPCPPPSFW 180
DB 121 ERGSYVRYNFMNDGFFLVKVTALTKQEDVVIPELPGQPVVICVFNWAFESCPCPPPSFW 180

QY 181 TGAALSSQGTPTTSHFSLVSFTPRPDHDTLTCHVDVFSKGVSAQRTVLRVAYAPRD 240
DB 181 TGAALSSQGTPTTSHFSLVSFTPRPDHDTLTCHVDVFSKGVSAQRTVLRVAYAPRD 240
QY 241 LVISIRSDNTPD----- 252
DB 241 LVISIRSDNTPALEPQPGNVVLEAQKQFRLRLCAADSPATLSWVLRVLSLSSHP 300
QY 253 -----PPENLRVMVSOANRTVLE 270
DB 301 WGRPLGLGLPGVKAGDSGRVTCBAENRIGSQOQALDLSVQYPPENLRVMVSOANRTVLE 360
QY 271 NLNGTSLPVLGGSLCLVCTHSSPPARLSWTORGQVLSQSPSDPGVLELPRVQVEHE 330
DB 361 NLNGTSLPVLGGSLCLVCTHSSPPARLSWTORGQVLSQSPSDPGVLELPRVQVEHE 420
QY 331 GEFTCHARHPLGSOHVSLSLVHY----- 354
DB 421 GEFTCHARHPLGSOHVSLSLVHYSPKLLGPSCSWEAEGHLCSSQASAPSLRWLGE 480
QY 355 -----X 355
DB 481 ELLEGSSQDSFEVTPSSAGFWANSSLSLHGLSSGLRLRCEAMNVHGAQSGSILQLPDK 540
QY 356 KGLISTAFSNGAFUGIGITALLFLCLALIIMKILPKERTOTETPRPFSRHSSTILDYINV 415
DB 541 KGLISTAFSNGAFUGIGITALLFLCLALIIMKILPKERTOTETPRPFSRHSSTILDYINV 600
QY 416 VPTAGPLAQKENQKATPNSPRTPLPPGAPSPESKKNQKQVQLPSPFPEPKSSTQAPESQ 475
DB 601 VPTAGPLAQKENQKATPNSPRTPLPPGAPSPESKKNQKQVQLPSPFPEPKSSTQAPESQ 660
QY 476 SOEELHVTATLNPFGVRPRPEARMKPGTQADYAEVKFQ 512
DB 661 SOEELHVTATLNPFGVRPRPEARMKPGTQADYAEVKFQ 697
RESULT 6
ADL82805
ID ADL82805 standard; protein; 697 AA.
XX
AC ADL82805;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human PRO71236, SEQ ID 7.
XX
KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
KW Gene Therapy; PRO; B cell related disorder; cancer;
KW immune-mediated inflammatory disease; human.
XX
OS Homo sapiens.
XX
PN WO2004024097-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029097.
XX
PR 16-SEP-2002; 2002US-0411392P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-329389/30.
DR N-PSDB; ADL82804.
XX
PT New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.

Claim 10; Fig 7; 695pp; English.

CC The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
CC antigen unresponsiveness, selective IgA deficiency, selective IgM
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.

Sequence 697 AA;

Query Match 95.2%; Score 2576.5; DB 8; Length 697;

Best Local Similarity 73.0%; Pred. No. 7.4e-195;

Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;

QY	1	MLLPILLSSLLGGSQAMDCGFWRVQESVMVPEGLCISVPCSFSPRQDWTGTPAYGYW	60
DB	1	MLLPILLSSLLGGSQAMDCGFWRVQESVMVPEGLCISVPCSFSPRQDWTGTPAYGYW	60
QY	61	FKAVTETTKGAPVATNHSQSEVEMSTRGRFQLTGDPKNGCSLVIRDAQMDESQYFFRV	120
DB	61	FKAVTETTKGAPVATNHSQSEVEMSTRGRFQLTGDPKNGCSLVIRDAQMDESQYFFRV	120
QY	121	ERGSYRYNFMNDGFFIKVTALTKQDDVYIPETLPGQVTVICVFNWAFESCPSPFSW	180
DB	121	ERGSYRYNFMNDGFFIKVTALTKQDDVYIPETLPGQVTVICVFNWAFESCPSPFSW	180
QY	181	TGAALSQGTPTTSHFSLVSLFTPRQDHTDLCVDFSRKGSVQRTVRLRVAYARD	240
DB	181	TGAALSQGTPTTSHFSLVSLFTPRQDHTDLCVDFSRKGSVQRTVRLRVAYARD	240
QY	241	LVISISRDNTPD-----	252
DB	241	LVISISRDNTPALEPQGNVPYLEAKQGLRLLCADSQPPATLSWLQNRVLSSSH	300
QY	253	-----PPENLRVMVQANRTVLE	270
DB	301	WGRPRLELPGVKAGDSGRYTCRANRLGSGQRAIDLVSQVPPENLRVMVQANRTVLE	360
QY	271	NLCNGTSLPVLGQSLCLVCTHSSPARLSWTQRQVLSPPQSDPGVLELPRVQVEHE	330
DB	361	NLCNGTSLPVLGQSLCLVCTHSSPARLSWTQRQVLSPPQSDPGVLELPRVQVEHE	420
QY	331	GETCHARPLGSHVLSLSVHY-----	354
DB	421	GETCHARPLGSHVLSLSVHYSPKLLGPGSCWDEAGLHCSCSSQASPAPSLRWLGE	480
QY	355	-----K	355
DB	481	ELLEGNSSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCANVHVGAGQSIIQLDPK	540
QY	356	KGLISTAFNGAFGLGIGITALLPLCLALIMKILPKRTQTTPRFRSRHSTIIDYINV	415
DB	541	KGLISTAFNGAFGLGIGITALLPLCLALIMKILPKRTQTTPRFRSRHSTIIDYINV	600
QY	416	VPTAGPLAOKRNOKATPNSPRTPLPGAPSBSKKNCKQYQLPSFPBPXSQTAPESQE	475
DB	601	VPTAGPLAOKRNOKATPNSPRTPLPGAPSBSKKNCKQYQLPSFPBPXSQTAPESQE	660
QY	476	SOBELHYATLNPFGVPRPRPEARMPKGTQADYAEVKFQ	512
DB	661	SOBELHYATLNPFGVPRPRPEARMPKGTQADYAEVKFQ	697

RESULT 7

ADD19314

ID ADD19314 standard; protein; 710 AA.

XX AC ADD19314;

XX 15-JAN-2004 (first entry)

XX Human secreted protein from gene 18 #3.

XX human secreted protein; cytostatic; antibacterial; virucide;

XX neuroprotective; gynaecological; gastrointestinal-Gen; cardiant;

XX cardiovascular-Gen; nephrotropic; antiinflammatory; muscular-Gen;

XX respiratory-Gen; immunosuppressive; cerebroprotective; vasotropic;

XX neutropic; antiallergic; cancer; bacterial infection; viral infection;

XX neural disorder; immune system disorder; blood disorder;

XX muscular disorder; reproductive disorder; gastrointestinal disorder;

XX pulmonary disorder; cardiovascular disorder; renal disorder;

XX inflammatory disorder; proliferative disorder; human.

XX Homo sapiens.

XX WO2003052377-A2.

XX 26-JUN-2003.

XX 06-NOV-2002; 2002WO-US035606.

XX 07-NOV-2001; 2001US-0331046P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPT; 2003-533050/50.

XX N-PSDB; ADD19239.

XX New isolated nucleic acids encoding signal transduction pathway component

XX polypeptides, useful for diagnosing, treating, and/or preventing

XX disorders such as cancer, infections, cardiovascular and inflammatory

XX diseases.

XX Claim 11; SEQ ID NO 141; 554pp; English.

XX The invention relates to an isolated nucleic acid molecule (cDNA)

XX encoding a human secreted protein, representing one of 85 novel genes.

XX Also included are recombinant vectors, host cells (expressing the

XX protein), the secreted proteins (including their fragments, epitopes and

XX homologues), an isolated antibody that binds specifically to the protein,

XX diagnosing a pathological condition or susceptibility to a pathological

XX condition (comprising determining the presence or absence of a mutation

XX in the nucleic acid and diagnosing a condition based on the presence or

XX absence of the mutation), diagnosing a pathological condition or

XX susceptibility to a pathological condition (comprising determining the

XX presence or amount of expression of the protein in a biological sample

XX and diagnosing a condition based on the presence or amount of expression

XX of the protein), preventing, treating or ameliorating a medical condition

XX by administering the nucleic acid or protein to a mammalian subject,

XX identifying a binding partner to the protein, the gene corresponding to

XX the cDNA sequence, and identifying an activity in a biological assay

XX (comprising expressing the nucleic acid in a cell, isolating the

XX supernatant, detecting an activity in a biological assay and identifying

XX the protein in the supernatant having the activity). The nucleic acids

XX and proteins display the following activities: Cytostatic, antibacterial,

XX Virucide, Neuroprotective, Gynaecological, Gastrointestinal-Gen,

XX Cardiant, Cardiovascular-Gen, Nephrotropic, Antiinflammatory, Muscular-

XX Gen, Respiratory-Gen, Immunosuppressive, Cerebroprotective, Vasotropic,

XX Neutropic, Antiallergic. The methods and compositions of the present

XX invention are useful for diagnosing, treating, preventing and/or

XX prognosticating disorders related to the novel polypeptides, such as

XX cancer, bacterial or viral infections, and neural, immune system, blood,


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253 -----PPENLRVWVQANRTVLE 270
243 WGRPLGLELPGVKAGDSGRYTCAENRLGSOQRALDLSVQYPPENLRVWVQANRTVLE 302
271 NLNGTSLPVLGQSICLVCTVTHSSPPARLSWTQRCQVLSQSPDPGVLELPRVQVEHE 330
303 NLNGTSLPVLGQSICLVCTVTHSSPPARLSWTQRCQVLSQSPDPGVLELPRVQVEHE 362
331 GEFTCHARPLGSHVLSLSVHYKGLISTAFSNGAFILGIGITALLFLCLALIIMKILP 390
363 GEFTCHARPLGSHVLSLSVHYKGLISTAFSNGAFILGIGITALLFLCLALIIMKILP 422
391 KRRTOTETPRPFSRHSITLDYINVVPTAGPLAQKNQKATPNSRPTPLPPGAPSPESKK 450
423 KRRTOTETPRPFSRHSITLDYINVVPTAGPLAQKNQKATPNSRPTPLPPGAPSPESKK 482
451 NOKKQVQLSPFPKSTQAPESQESQEBLHYATLNFGRPRPBARMEKGTQADYAEVK 510
483 NOKKQVQLSPFPKSTQAPESQESQEBLHYATLNFGRPRPBARMEKGTQADYAEVK 542
511 FQ 512
543 FQ 544

RESULT 9
AAV41724
ID AAV41724 standard; protein; 544 AA.
XX
XX AAV41724;
XX
XX 07-DEC-1999 (first entry)
XX
XX Human PR0940 protein sequence.
XX
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein.
XX
XX Homo sapiens.
XX
XX WC9946281-A2.
XX
XX 16-SEP-1999.
XX
XX 08-MAR-1999; 99MO-US0005028.
XX
XX 10-MAR-1998; 98US-0077450P.
XX
XX 11-MAR-1998; 98US-0077632P.
XX
XX 11-MAR-1998; 98US-0077641P.
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XX 11-MAR-1998; 98US-0077649P.
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XX 12-MAR-1998; 98US-0077791P.
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XX 13-MAR-1998; 98US-0078004P.
XX
XX 17-MAR-1998; 98US-00040220.
XX
XX 20-MAR-1998; 98US-0078886P.
XX
XX 20-MAR-1998; 98US-0078910P.
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XX 20-MAR-1998; 98US-0078936P.
XX
XX 20-MAR-1998; 98US-0078939P.
XX
XX 25-MAR-1998; 98US-0079294P.
XX
XX 26-MAR-1998; 98US-0079656P.
XX
XX 27-MAR-1998; 98US-0079663P.
XX
XX 27-MAR-1998; 98US-0079664P.
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XX 27-MAR-1998; 98US-0079689P.
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XX 27-MAR-1998; 98US-0079728P.
XX
XX 27-MAR-1998; 98US-0079786P.
XX
XX 30-MAR-1998; 98US-0079920P.
XX
XX 30-MAR-1998; 98US-0079923P.
XX
XX 31-MAR-1998; 98US-0080105P.
XX
XX 31-MAR-1998; 98US-0080107P.
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XX 31-MAR-1998; 98US-0080165P.
XX
XX 31-MAR-1998; 98US-0080194P.
XX
XX 01-APR-1998; 98US-0080327P.

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PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082588P.
PR 21-APR-1998; 98US-0082589P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082757P.
PR 23-APR-1998; 98US-0082736P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083332P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 30-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084588P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.

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(GETH) GENENTECH INC.

Wood WT, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.

N-ESDB; AAZ34109.

New secreted and transmembrane polypeptides and their polynucleotides,
useful for treating blood coagulation disorders, cancers and cellular


```

DB 61 FKAATETTKGAPVATNHSREVENSTGRFQLTGDPAKGNCSLVIRDAQMDESQYFFRV 120
DB 121 ERGSYVRYNFMNDGFLKVTALTQKDDVPIPELFGQPVTVICVFNWAFESCPSPFSW 180
DB 121 ERGSYVRYNFMNDGFLKVT----- 140
DB 181 TGAALSSQGTKPTTSHFSVLSFTPRQDHDITLCHVDSRKGVSAQRTVRLVAVAPRD 240
DB 141 -----VLSFTPRQDHDITLCHVDSRKGVSAQRTVRLVAVAPRD 182
DB 241 LVISIRSDNTPD----- 252
DB 183 LVISIRSDNTPALEPQPGQNVVYLEAQKQFLFLLCAADSQPPATLSWVLQNRVLSSSH 242
DB 253 -----PPENLRVWVQAQNTVLE 270
DB 243 WGRPRPLGLELPYKAGDSGRYTCEAENRLGSCQQRALDLSVOYPPENLRVWVQAQNTVLE 302
DB 271 NLNGTSLPVLGQSLCLVCTHSSPPARLSWTQRCQVLSQPSQSPDGVLELPRVQVEHE 330
DB 303 NLNGTSLPVLGQSLCLVCTHSSPPARLSWTQRCQVLSQPSQSPDGVLELPRVQVEHE 362
DB 331 GFTCHARHPLGSHVLSLSVHYKGLISTAFSGAFIGITALLFLCLALITMKILP 390
DB 363 GFTCHARHPLGSHVLSLSVHYKGLISTAFSGAFIGITALLFLCLALITMKILP 422
DB 391 KRRTQETPRPRESHTILDYINVVPTAGPLAQKRNQATPNSRPTPLPPGAPSPESKK 450
DB 423 KRRTQETPRPRESHTILDYINVVPTAGPLAQKRNQATPNSRPTPLPPGAPSPESKK 482
DB 451 NQKKQVQLSPFPKSTQAPESQESBELHYATLNFGRVPRPEARMKGTQADYAEVK 510
DB 483 NQKKQVQLSPFPKSTQAPESQESBELHYATLNFGRVPRPEARMKGTQADYAEVK 542
DB 511 FQ 512
DB 543 FQ 544

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RESULT 11

AAU29082
ID AAU29082 standard; protein; 544 AA.

AAU29082;

18-DEC-2001 (first entry)

Human PRO polypeptide sequence #59.

PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

Homo sapiens.

WO2001.68848-A2.

20-SEP-2001.

28-FEB-2001; 2001WO-US006520.

01-MAR-2000; 2000WO-US005601.

02-MAR-2000; 2000WO-US005841.

03-MAR-2000; 2000US-0187202P.

06-MAR-2000; 2000US-0186568P.

14-MAR-2000; 2000US-0189320P.

14-MAR-2000; 2000US-0189328P.

21-MAR-2000; 2000WO-US006884.

21-MAR-2000; 2000US-0191314P.
28-MAR-2000; 2000US-0192655P.
29-MAR-2000; 2000US-0193032P.
29-MAR-2000; 2000US-0193053P.
30-MAR-2000; 2000WO-US008439.
04-APR-2000; 2000US-0194449P.
11-APR-2000; 2000US-0195975P.
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25-APR-2000; 2000US-0199397P.
25-APR-2000; 2000US-0199550P.
03-MAY-2000; 2000US-0199654P.
03-MAY-2000; 2000US-0201516P.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014942.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
05-JUN-2000; 2000US-0209832P.
28-JUL-2000; 2000WO-US020710.
22-AUG-2000; 2000US-00644848.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WO-US034956.
(GETH) GENENTECH INC.
Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
WPI; 2001-602746/68.
N-PSDB; AAS45983.
Novel nucleic acids encoding PRO polypeptides, used to diagnose the
presence of tumors, such as prostate and breast tumors, in mammals and to
screen for modulators of the compounds.
Claim 11; Fig 11B; 774pp; English.
Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to
detect the presence of a tumour in a mammal by comparing the level of
expression of a PRO polypeptide in a test sample of cells from the animal
and a control sample of normal cells, whereby a higher level of
expression in the test sample indicates the presence of a tumour in the
mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
and rabbits but are preferably human. The polypeptides can be used to
stimulate tumour necrosis factor (TNF) alpha release from human blood,
when contacted with it. A specific polypeptide can be used to stimulate
the proliferation or differentiation of chondrocyte cells. The PRO
proteins can be used to determine the presence of tumours and also
susceptibility to tumour development, particularly adrenal, lung, colon,
breast, prostate, cervical, or liver tumours, in mammalian
subjects. The oligonucleotide probes specific for the PRO nucleic acids
can be used for genetic analysis of individuals with genetic disorders

Sequence 544 AA;

Query Match

Best Local Similarity 83.7%; Score 2265; DB 4; Length 544;

Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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Db

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Qy	241	LVISISRONTPD-----	252
Db	183	LVISISRONTPALEPQPOQNVYLEAQKQFLRLCAADSQPPATLSWVLQNRVLSSSH	242
Qy	253	-----PPENLRVMYSQANRTVLE	270
Db	243	WCPRELGLELPCVKAGDSGRVTCRAENRLGSOQRALDLSVQYPPENLRVMYSQANRTVLE	302
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Db	303	NLNGNTSLFVLEQSLCLVCTHVSPPARLSWTQRQVLSQPSQSDPGVLELPRVQVEHE	362
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Qy	391	KRTQTETPRFRSHSTILDYINVVPTAGPLAQRNKAQNPSPRTPLPFCAPSPESSK	450
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KW	KW	dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;	
KW	KW	antibody-dependent enzyme mediated prodrug therapy.	
XX	OS	Homo sapiens.	
XX	PN	US2003027272-A1.	
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XX	PF	21-JUN-2002; 2002US-00176492.	
XX	PR	18-SEP-1997; 97US-0059263P.	
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07-OCT-1998; 98US-00168978.

Query Match 83.7%; Score 2265; DB 6; Length 544;
Best Local Similarity 74.8%; Pred. No. 2.4e-170;
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ABU8006
ID ABU8006 standard; protein; 544 AA.
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AC ABU8006;
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DT 07-JUL-2003 (first entry)
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DE DE Novel human secreted and transmembrane protein PR0940.
XX
KW Human; secreted and transmembrane protein: PRO; Gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX
PD 13-FEB-2003.
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PF 26-JUN-2002; 2002US-00183012.
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PR 18-SEP-1997; 97US-0059263P.
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Query Match 83.7%; Score 2265; DB 6; Length 544;
Best Local Similarity 74.8%; Pred. No. 2, 4e-170;
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61 FKAVTETTKGAPVATHQREVMSTGRFQLTGDPKNCNCSLVIRDAQMDQESYFRV 120
61 FKAVTETTKGAPVATHQREVMSTGRFQLTGDPKNCNCSLVIRDAQMDQESYFRV 120
121 ERGSYVYNFMNDGFFLKVTALTQKPDVYIPETLEFGQPVTVICVFNWAFERCPPPFSW 180
121 ERGSYVYNFMNDGFFLKVT----- 140
181 TGAALSSQSKTPTTSFSLFTPRQDHTDLTCHVDPSKGVSAQRTVRLVAVAPRD 240

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141 Db -----VLSFTPRQDHTDLTCHVDPSKGVSAQRTVRLVAVAPRD 182
241 QY LVISIRDNTPD----- 252
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253 QY -----PPENLRVMVMSQANRTVLE 270
243 Db WGPRLGLELPGVKAGDSGRYTCRAENRGLSQQRALDLSVQYPPENLRVMVMSQANRTVLE 302
271 QY NLNGTSLPVLGOSLCLVCVTHSSPPARLSWTORGQVLSPSPSDPVLPRVQVEHE 330
303 Db NLNGTSLPVLGOSLCLVCVTHSSPPARLSWTORGQVLSPSPSDPVLPRVQVEHE 362
331 QY GEFTCHARHPLGSOHVSLSVHYKGLISTAFNGAFLGIGITALLFLCLALIMKILP 390
363 Db GEFTCHARHPLGSOHVSLSVHYKGLISTAFNGAFLGIGITALLFLCLALIMKILP 422
391 QY KRTQTETPRPRSRHSTILDYINNVPTAGPLAQKRNQKATPNSPRTPLPFGAPSPESKK 450
423 Db KRTQTETPRPRSRHSTILDYINNVPTAGPLAQKRNQKATPNSPRTPLPFGAPSPESKK 482
451 QY NOKKOYOLPSFPPEKSTQAPESQESOEELHYATLNFPGVPRPEARMKGTQADYAEVK 510
483 Db NOKKOYOLPSFPPEKSTQAPESQESOEELHYATLNFPGVPRPEARMKGTQADYAEVK 542
511 QY FQ 512
543 Db FQ 544

RESULT 14
ABU84321
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XX AC ABU84321;
XX DT 02-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #59.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX KW tissue typing.
XX OS Homo sapiens.
XX PN US2003032112-A1.
XX PD 13-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176756.
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PR 04-OCT-1998; 98US-0102965P.
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Query Match 83.7%; Score 2265; DB 6; Length 544;
Best Local Similarity 74.8%; Pred. No. 2.4e-170;
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DB 61 FKAVTTTGAPVATNQREVEMSTRGRFQLTGDPKGNCSLVIRDAQMDESQYFRV 120
QY 121 ERGSVYVYPMNDGFFLKVTALTQKDVPIPELEPQVPTVICVFNWAFESCPPPSFW 180
DB 121 ERGSVYVYPMNDGFFLKVT ----- 140
QY 181 TGAALSSQGTPTTSHFSLVPTPRQDHDHDLTCHVDFSRKGVSAQRTVRLVAYAPRD 240
DB 141 -----VLSPTPRQDHDHDLTCHVDFSRKGVSAQRTVRLVAYAPRD 182
QY 241 LVISISRDNTPD ----- 252
DB 183 LVISISRDNTPALEPOQGNVFLYEAQKQFLRLCAADSQPPATLSWVLQNRVLSSHP 242
QY 253 -----PPENLRVWVSCANRTVLE 270
DB 243 WGRPLGLELPGVKAGDSGRYTCRAENRLGSGQORALDLSQYPPENLRVWVSCANRTVLE 302
QY 271 NLNGTSLVLEQSLCLVCVTHSSPPARLSWTQRCQVLSQSPQSDPGVLELPRVQVEHE 330
DB 303 NLNGTSLVLEQSLCLVCVTHSSPPARLSWTQRCQVLSQSPQSDPGVLELPRVQVEHE 362
QY 331 GEFTCHARPLGSHVLSLSVHYKGLISTAFSNGAFIGITALLFLCLALIIIMKILP 390
DB 363 GEFTCHARPLGSHVLSLSVHYKGLISTAFSNGAFIGITALLFLCLALIIIMKILP 422
QY 391 KRRTOTETPRPRFSRSTILDYINVVPTAGLAQRNOKATNSPRTPLPGAPSPESKK 450
DB 423 KRRTOTETPRPRFSRSTILDYINVVPTAGLAQRNOKATNSPRTPLPGAPSPESKK 482
QY 451 NOKKQYOLSPFPKSTQAPESQESQELHATLNFPGVRPRPEARMPKGTQADYAEVK 510
DB 483 NOKKQYOLSPFPKSTQAPESQESQELHATLNFPGVRPRPEARMPKGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

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RESULT 15

ABR66195

ID ABR66195 standard; protein; 544 AA.

AC

ABR66195;

EX

DATE 05-AUG-2003 (first entry)

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DE Human secreted polypeptide PRO940, SEQ ID NO:118.

XX Human; PRO; secreted protein; transmembrane protein;

KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;

KW chondrocyte; proliferation; differentiation; cartilage disorder;

KW bone disorder; arthritis; sports injury; cancer; diagnosis;

KW adrenal tumour; lung; colon; breast; prostate; kidney; cervix;

KW liver; drug screening; transgenic animal; genetic analysis;

KW antiarthritic; vulnery; gene therapy.

XX Homo sapiens.

OS US2003027278-A1.

PN 06-FEB-2003.

PD 21-JUN-2002; 2002US-00176987.

PR 18-SEP-1997; 97US-0059283P.

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PR 17-OCT-1997; 97US-0062250P.

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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
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Best Local Similarity 74.8%; Pred. No. 2.4e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
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QY 121 ERGSYVRVNFMDGFFLTKVDVITPETLEPGQPVTVICVFNWAFEECPSPFSW 180
Db 121 ERGSYVRVNFMDGFFLTKVDVITPETLEPGQPVTVICVFNWAFEECPSPFSW 180
QY 181 TGAALSSQGTKTPTTSHFSVLSTFRPQDHTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
Db 141 -----VLSFTPRQDHTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182
QY 241 LVISIRDNTPD----- 252
Db 183 LVISIRDNTPALEPQCGNVPLYEAKQGFRLLLCAADQPPATLSWLVQNRVLSHP 242
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QY 253 -----PPENLRVMVSQANRTVLE 270
DB 243 WGRPLGLELPVKGAGDSGRYTCAENRLGSOORALDLSVQYPPENLRVMVSQANRTVLE 302
QY 271 NLGNSTSLPVLEQSLCLVCVTHSSPPARLSWTQRCQVLSPOPSDPGVLELPRVQVEHE 330
DB 303 NLGNSTSLPVLEQSLCLVCVTHSSPPARLSWTQRCQVLSPOPSDPGVLELPRVQVEHE 362
QY 331 GEFTCHARHPLGSOHVLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIMKILP 390
DB 363 GEFTCHARHPLGSOHVLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIMKILP 422
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DB 423 KRRTQETPRPRESRHSITLDYINVVPTAGPLAQKNOKATNSPRTPLPGAPSPESKK 482
QY 451 NQKKQYQLPSFPPEPKSGSTQAFESQESQEBLHYATLNFPGVRPRPEARMKPGTQADYAEVK 510
DB 483 NQKKQYQLPSFPPEPKSGSTQAFESQESQEBLHYATLNFPGVRPRPEARMKPGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

Search completed: November 5, 2004, 13:53:22
Job time : 65.6073 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:53:32 ; Search time 88.0765 Seconds
(without alignment)
2053.348 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2580.5	95.4	697	10	US-09-910-600-28
2	2576.5	95.2	697	10	US-09-984-130-149
3	2576.5	95.2	697	15	US-10-403-938-7
4	2576.5	95.2	697	16	US-10-614-853-10
5	2278	84.2	544	10	US-09-910-600-8
6	2265	83.7	544	9	US-09-978-295A-259
7	2265	83.7	544	9	US-09-978-697-259
8	2265	83.7	544	9	US-09-978-192A-259
9	2265	83.7	544	9	US-09-999-832A-259
10	2265	83.7	544	10	US-09-978-188A-259
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ALIGNMENTS

RESULT 1
US-09-910-600-28
; Sequence 28, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,139
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L3-995-2
US-09-910-600-28

Query Match 95.4%; Score 2580.5; DB 10; Length 697;
Best Local Similarity 73.2%; Pred. No. 1e-177;
Matches 510; Conservative 1; Mismatches 1; Indels 185; Gaps 2;

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Db 1 MLLPLLSSLLGGSQAMDGRFWIRVQSVVMVPEGLCISVPCSFSPRPQDWTGSTPAYGYW 60

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DB 361 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQRGQVLSPOSPDPGVLELPRVQVEHE 420
QY 331 GEFTCHARHPLGSOHVSLSLVHY 354
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RESULT 2

US-09-984-130-149
Sequence 149, Application US/09984130
Publication No. US2003005231A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PP489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 09/836,353
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 149
LENGTH: 697
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-130-149

Query Match 95.2%; Score 2576.5; DB 10; Length 697;

Best Local Similarity 73.0%; Pred. No. 2e-177; 2; Indels 185; Gaps 2;
Matches 509; Conservative 1; Mismatches 2

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DB 361 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQRGQVLSPOSPDPGVLELPRVQVEHE 420
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DB 541 KGLISTAFNGAFGLGIGITALLELCLALIMKILPKRTOTETPRFRSRHTILDYINV 600
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DB 661 SOBELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 697

RESULT 3

US-10-403-938-7
Sequence 7, Application US/10403938
Publication No. US20040025195A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
TITLE OF INVENTION: BGS-19
FILE REFERENCE: D0227 NP
CURRENT APPLICATION NUMBER: US/10/403,938
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: U.S. 60/368,422
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 697
TYPE: PRT
ORGANISM: Homo sapiens
US-10-403-938-7

Query Match 95.2%; Score 2576.5; DB 15; Length 697;

Best Local Similarity 73.0%; Pred. No. 2e-177; 2; Indels 185; Gaps 2;
Matches 509; Conservative 1; Mismatches 2

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DB 1 MLLPLLSSLLGSGQAMGRFIRVOESVWVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
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DB 61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
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DB 661 SQEELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 697

RESULT 4

US-10-614-853-10

; Sequence 10, Application US/10614853

; Publication No. US20040138114A1

; GENERAL INFORMATION:

; APPLICANT: HENRY CHIU

; APPLICANT: HILARY CLARK

; APPLICANT: KATHRYN DENNIS

; APPLICANT: SHERMAN FONG

; APPLICANT: JILL SCHOENFELD

; APPLICANT: WILLIAM WOOD

; APPLICANT: THOMAS WU

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE

; FILE REFERENCE: P1973R1-US

; CURRENT APPLICATION NUMBER: US/10/614,853

; CURRENT FILING DATE: 2003-07-08

; PRIOR APPLICATION NUMBER: US 60/394,485

; PRIOR FILING DATE: 2002-07-08

; NUMBER OF SEQ ID NOS: 28

; SEQ ID NO 10

; LENGTH: 697

; TYPE: PRT

; ORGANISM: Homo sapien
US-10-614-853-10

Query Match 95.2%; Score 2576.5; DB 16; Length 697;

Best Local Similarity 73.0%; Pred. No. 2e-177;

Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;

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DB 1 MLLPLLSSLLGSGQAMGRFIRVOESVWVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
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QY 121 ERGSVYRNFMDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPSPFSW 180
DB 121 ERGSVYRNFMDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPSPFSW 180
QY 181 TGAALSSQGTKTTHSFVLSFTPRPDHDTLTCHVDFSRKGVSAQRTVRLRAYAPRD 240
DB 181 TGAALSSQGTKTTHSFVLSFTPRPDHDTLTCHVDFSRKGVSAQRTVRLRAYAPRD 240
QY 241 LVISISRDNTPD----- 252
DB 241 LVISISRDNTPALEPQPOGNVPLYEAQKQFLRLCAADSPATLSWVQNRLVSSHP 300
QY 253 ----- 270
DB 301 WGRPLGLELPGVKAGDSGRYTCRAENRLGSGQORALDLSVQYPPENLRVMVSOANRTVLE 360
QY 271 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTORGQVLSQPSQSDPGVLELPRVQVEHE 330
DB 361 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTORGQVLSQPSQSDPGVLELPRVQVEHE 420
QY 331 GEFTCHARPLGSGHVLSLSVHY----- 354
DB 421 GEFTCHARPLGSGHVLSLSVHYSPKLLGPSCSWEAEGHLCSSQASAPSLRWLGE 480
QY 355 -----K 355
DB 481 ELLEGNSQDSFEVTPSSAGPWANSLSLHGLSSGLRLRCEANVHGAQSGSILQLPDK 540
QY 356 KGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRRTOTETPRFRSHSTILDYINV 415
DB 541 KGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRRTOTETPRFRSHSTILDYINV 600
QY 416 VPTAGPLAQRNOKATPNSPRTPLPGAPSPSKKNQKQYQLPSPFPKSKSTQAPESQE 475
DB 601 VPTAGPLAQRNOKATPNSPRTPLPGAPSPSKKNQKQYQLPSPFPKSKSTQAPESQE 660
QY 476 SQEELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 512
DB 661 SQEELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 697

RESULT 5

US-09-910-600-8

; Sequence 8, Application US/09910600

; Publication No. US20030036631A1

; GENERAL INFORMATION:

; APPLICANT: Longphre, Malinda

; APPLICANT: Chang, Han

; APPLICANT: Whitney, Gena

; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF

; FILE REFERENCE: D0003NP

; CURRENT APPLICATION NUMBER: US/09/910,600

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: 60/220,139

; PRIOR FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

LENGTH: 544

TYPE: PRT

ORGANISM: Homo sapiens

US-937-636-3

Query Match

Best Local Similarity 84.2%; Score 2278; DB 10; Length 544;

Matches 452; Conservative 1; Mismatches 1; Indels 148; Gaps 2;

1 MLPLLLSSLLGSGQAMGRFWIRVOESVWVPEGLCISVPCSFSPRODWTGSTAYGW 60
1 MLPLLLSSLLGSGQAMGRFWIRVOESVWVPEGLCISVPCSFSPRODWTGSTAYGW 50
61 FKAIVTTTGAPVATNHQREVEMSTRGRFQLTGDPAKNGCSLVIRDAQMDESQYFRV 120
61 FKAIVTTTGAPVATNHQREVEMSTRGRFQLTGDPAKNGCSLVIRDAQMDESQYFRV 120
121 ERGSYVRYNFMNDGFFLKVTALTKQPDVYIPETLEPGQPVTVICVFNWAFESCPCPPSSW 180
121 ERGSYVRYNFMNDGFFLKVT----- 140
181 TGAALSSQGTPTTSHFSLVFTPRQDHDHDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
181 TGAALSSQGTPTTSHFSLVFTPRQDHDHDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182
141 -----VLSTFTPRQDHTDITLCHVDFSRKGVSAQRTVRLRVAYAPRD 252
241 LVLSISRDNTPD----- 270
183 LVLSISRDNTPALPEPOQGNVPLEAQKQFLLLCAADSQPPATLSWYLNRLVLSHP 242
253 -----PPENLRVWVSAQNRVTLE 270
243 WGRPLGLPLGVKAGDSGRYTCENRNLGSCQALDLSVQYFPPENLRVWVSAQNRVTLE 302
271 NLNGTSLPVEQSCJCLVCTHSSPRLSWTORQVLSQPSQSDPGVLELPRVQVEHE 330
303 NLNGTSLPVEQSCJCLVCTHSSPRLSWTORQVLSQPSQSDPGVLELPRVQVEHE 362
331 GEFTCHARPLGSHVLSLSVHYKGLISTAFNSCAFILGIGITALLFLCLALIIMKILP 390
363 GEFTCHARPLGSHVLSLSVHYKGLISTAFNSCAFILGIGITALLFLCLALIIMKILP 422
391 KRITQETPRPFSRHSITLDYINVVPTAGPLAQKNQKATPNSPRTELPQCAPSPESKK 450
423 KRITQETPRPFSRHSITLDYINVVPTAGPLAQKNQKATPNSPRTELPQCAPSPESKK 482
451 NQKQYQLSFPFKSSTQAPESQESQELHYATLNFGRVSRPERBMPKGTQADYAEVK 510
483 NQKQYQLSFPFKSSTQAPESQESQELHYATLNFGRVSRPERBMPKGTQADYAEVK 542
511 FQ 512
543 FQ 544

RESULT 6

US-09-978-295A-259

Sequence 259, Application US/09978295A

Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 1997-11-13
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 / PRIOR APPLICATION NUMBER: 60/085579
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085580
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085573
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085704
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 9; Length 544;
 Best Local Similarity 74.8%; Pred. No. 4.6e-55;
 Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

Qy	1	MLP	LLSSLLGGSQAMDGRFWIRVOESVMVPEGLCISVPCSPSYPRQDWTGTTPAYGYW	60
Db	1	MLP	LLSSLLGGSQAMDGRFWIRVOESVMVPEGLCISVPCSPSYPRQDWTGTTPAYGYW	60
Qy	61	FXAVT	TTKGAPVATNHQSRREVEMSTGRFQLTGDPKAGNCSLVIRDAQMDSEQYFVRV	120
Db	61	FXAVT	TTKGAPVATNHQSRREVEMSTGRFQLTGDPKAGNCSLVIRDAQMDSEQYFVRV	120
Qy	121	ERGSY	VRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPFSW	180
Db	121	ERGSY	VRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPFSW	180
Qy	181	TGAAL	SSQGTKPTTSHFSVLSTPRPDQDHTDILCHVDPSRKGVSQRTVRLVAYAPRD	240
Db	141	-----	-----VLSTPRPDQDHTDILCHVDPSRKGVSQRTVRLVAYAPRD	182
Qy	241	LVISIS	RDNTPD-----	252
Db	183	LVISIS	RDNTPALEFPQCGNVPLYEAKQGFLLCAADSQPPATLSWVLQNRVLSSSH	242
Qy	253	-----	-----PPENLRVMVSOANRTVLE	270
Db	243	WGPR	PLGLFPGVKAGDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLE	302
Qy	271	NLNG	TSLPVLEGOSLVCVTHSSPPARLSWTORGVLSPSPSDPGVLELPRVQVEHE	330
Db	303	NLNG	TSLPVLEGOSLVCVTHSSPPARLSWTORGVLSPSPSDPGVLELPRVQVEHE	362
Qy	331	GEFT	CHARHPLGSHVSLSVHYKGLISTAFSNGAFLGIGITALLFLCLAIINKILP	390
Db	363	GEFT	CHARHPLGSHVSLSVHYKGLISTAFSNGAFLGIGITALLFLCLAIINKILP	422

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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078886
423 KRRTQETPRPSRHSHTILDYINVVPTAGPLAQKRNQKATNSPRTPLPPGAPSPESKK 482
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
451 NKKQYQLSPFPKPKSTQAPESQESQEBLHYATLNFPGVRPRPMPKGTQADYAEVK 510
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
483 NKKQYQLSPFPKPKSTQAPESQESQEBLHYATLNFPGVRPRPMPKGTQADYAEVK 542
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
QY 511 FQ 512
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
Db 543 FQ 544
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
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PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
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PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700

US-09-978-697-259
Sequence 259, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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3	PRIOR FILING DATE: 1998-04-22	
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59	PRIOR FILING DATE: 1998-05-15	
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61	PRIOR FILING DATE: 1998-05-15	
62	PRIOR APPLICATION NUMBER: 60/085579	
63	PRIOR FILING DATE: 1998-05-15	
64	PRIOR APPLICATION NUMBER: 60/085580	
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67	PRIOR FILING DATE: 1998-05-15	
68	PRIOR APPLICATION NUMBER: 60/085704	
69	PRIOR FILING DATE: 1998-05-15	
70	PRIOR APPLICATION NUMBER: 60/085697	

Query Match 83.7%; Score 2265; DB 9; Length 544;
Best Local Similarity 74.8%; Pred. No. 4.6e-155;

Matches	450;	Conservative	1;	Mismatches	3;	Indels	148;	Gaps	2
Qy	1	MLPLLLSLLGSGQAMDRFWIRVOESVMVPGGLCISVPDCSPSYPRQDWTGSTPAYGYW	60						
Db	1	MLPLLLSLLGSGQAMDRFWIRVOESVMVPGGLCISVPDCSPSYPRQDWTGSTPAYGYW	60						
Qy	61	FKAVTETTKGAPVATNHQSREVMSRTRGFQLTGDPKAGNCSLVIRDAQMDESOYFRV	120						
Db	61	FKAVTETTKGAPVATNHQSREVMSRTRGFQLTGDPKAGNCSLVIRDAQMDESOYFRV	120						
Qy	121	ERGSYYRYNPMNDGFFLKVTALTQKPDDVIPELTLEPGQPVTVICFVNFAFECCPPPSFW	180						
Db	121	ERGSYYTYNPMNDGFFLKVT-----	140						
Qy	181	TGAALSSQGKTPTSHEFSVLSTPRPODHDTDLTCHVDPSRKGVSAORTVRLRVAYAPRD	240						
Db	141	-----VLSFTPRPDHNTDUTCHVDPSRKGVSAORTVRLRVAYAPRD	182						
Qy	241	LVISISRDNTPD-----	25						
Db	183	LVISISRDNTPALEPQGNPNVLEAQGOFLALLCAADSQPPATLTSWLQNRLVSSSHP	242						
Qy	253	-----PPENLRVMVSQAANRTVLE	270						
Db	243	WGPRPLGLELPVKAGDSGRYT CRAENRLGSGQRALDSLVOYPPENLRVMVSQAANRTVLE	302						
Qy	271	NLNGHTSLPVLEGOSLCVCVTHSSPPARLSWTORGQOVLSPSQSDPFGVLELPRVQVEHE	330						
Db	303	NLNGHTSLPVLEGOSLCVCVTHSSPPARLSWTORGQOVLSPSQSDPFGVLELPRVQVEHE	362						
Qy	331	GETTCARHPLOGSHVLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP	390						
Db	363	GETTCARHPLOGSHVLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP	422						
Qy	391	KRTQTETPRPRSRSHTIILDYINNVPTAGLAQKNOKATPNSPRTPLPFGAPSPSKK	450						
Db	423	KRTQTETPRPRSRSHTIILDYINNVPTAGLAQKNOKATPNSPRTPLPFGAPSPSKK	482						
Qy	451	NQQKQYQLPFPPFKSSTQAPESQSEELHYATLNPPGVVRPEARMPKGTQADYAEVK	510						
Db	483	NQQKQYQLPFPPFKSSTQAPESQSEELHYATLNPPGVVRPEARMPKGTQADYAEVK	542						
Qy	511	FQ 512							
Db	543	FQ 544							
 RESULT 8 US-09-978-192A-259 ; Sequence 259, Application US/09978192A ; Patent No. US2002017753A1 ; GENERAL INFORMATION: ; APPLICANT: Ashkenazi, Avi ; APPLICANT: Baker Kevin P. ; APPLICANT: Botstein, David ; APPLICANT: Desnovers, Luc ; APPLICANT: Eaton, Dan ; APPLICANT: Ferrara, Napoleon ; APPLICANT: Filvaroff, Ellen ; APPLICANT: Fong, Sherman ; APPLICANT: Gao, Wei-Qiang ; APPLICANT: Gerber, Hanspeter ; APPLICANT: Gerritsen, Mary E. ; APPLICANT: Goddard, Audrey ; APPLICANT: Godowski, Paul J. ; APPLICANT: Grimaldi, J. Christopher ; APPLICANT: Gurney, Austin L. ; APPLICANT: Hillan, Kenneth J. ; APPLICANT: KJ-javin, Ivar J. ; APPLICANT: Kuo, Sophia S. ; APPLICANT: Napier, Mary A. ; APPLICANT: Pan, James; ; APPLICANT: Paoni, Nicholas F.									

APPLICANT: Roy, Margaret Ann	7	PRIOR APPLICATION NUMBER: 60/080333
APPLICANT: Shelton, David L.	7	PRIOR FILING DATE: 1998-04-01
APPLICANT: Stewart, Timothy A.	7	PRIOR APPLICATION NUMBER: 60/081070
APPLICANT: Tumas, Daniel	7	PRIOR FILING DATE: 1998-04-08
APPLICANT: Williams, P. Mickey	7	PRIOR APPLICATION NUMBER: 60/081049
APPLICANT: Wood, William I.	7	PRIOR FILING DATE: 1998-04-08
TITLE OF INVENTION: Scratched and Transmembrane Polypeptides and Nucleic	7	PRIOR APPLICATION NUMBER: 60/081071
TITLE OF INVENTION: Acids Encoding the Same	7	PRIOR FILING DATE: 1998-04-08
FILE REFERENCE: P2630PIC9	7	PRIOR APPLICATION NUMBER: 60/081195
CURRENT APPLICATION NUMBER: US/99/978,192A	7	PRIOR FILING DATE: 1998-04-08
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PRIOR APPLICATION NUMBER: 09/18585	7	PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 2001-07-30	7	PRIOR APPLICATION NUMBER: 60/081229
PRIOR APPLICATION NUMBER: 60/062250	7	PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1997-10-17	7	PRIOR APPLICATION NUMBER: 60/081955
PRIOR APPLICATION NUMBER: 60/064249	7	PRIOR FILING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-03-12	7	PRIOR APPLICATION NUMBER: 60/082804
PRIOR APPLICATION NUMBER: 60/078004	7	PRIOR FILING DATE: 1998-04-22
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PRIOR APPLICATION NUMBER: 60/078886	7	PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-03-25	7	PRIOR APPLICATION NUMBER: 60/083392
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PRIOR APPLICATION NUMBER: 60/080105	7	PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/080107	7	PRIOR FILING DATE: 1998-04-30
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PRIOR FILING DATE: 1998-04-01	7	PRIOR APPLICATION NUMBER: 60/084639
PRIOR APPLICATION NUMBER: 60/080333	7	PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-04-01	7	PRIOR APPLICATION NUMBER: 60/084640

;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
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;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 9; Length 544;

Best Local Similarity 74.8%; Pred. No. 4, 6e-155; Indels 148; Gaps 2;
Matches 450; Conservative 1; Mismatches 3;

QY 1 MLLPILLSLLGSGQAMGDRFIRVQESVMVPEGLICISVPCSFSPRODWTGSPAYGYW 60
DB 1 MLLPILLSLLGSGQAMGDRFIRVQESVMVPEGLICISVPCSFSPRODWTGSPAYGYW 60
QY 61 FXAVTETTKGAVATNHQSRVEMSTRGFTQTPAKGNCSLVIRDAQMDQESYFFRV 120
DB 61 FXAVTETTKGAVATNHQSRVEMSTRGFTQTPAKGNCSLVIRDAQMDQESYFFRV 120
QY 121 ERGSYRVNFMNDGFFLKVTALTQKPDVYIPETLEFGQPVTVICVFNWAFEECPPEPSW 180
DB 121 ERGSYRVNFMNDGFFLKVT-----VLSTPRPDHNTDLTCHVDFSRKGVSAQRTVLRVAYAPRD 140
QY 181 TGAALSSQGTKESTSHFSVLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVLRVAYAPRD 240
DB 141 -----VLSTPRPDHNTDLTCHVDFSRKGVSAQRTVLRVAYAPRD 182
QY 241 LVISISRDNTPD----- 252
DB 183 LVISISRDNTPALEPOQPNVYLEAQKQFLRLLLCAADSQPPATLSWVLQNRVLSSHP 242
QY 253 -----PPENLRVMVSOANRTVLE 270
DB 243 WGPRLPIGLPGVXAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVMVSOANRTVLE 302
QY 271 NLNGTSLVLEGGOSLCLVCTHSSPPARLSWTQGVLSQSDPGVLELPRVQVEHE 330
DB 303 NLNGTSLVLEGGOSLCLVCTHSSPPARLSWTQGVLSQSDPGVLELPRVQVEHE 362
QY 331 GFETCHARPLGOSQVLSLSVHYKGLISTAFSNGAFGLIGITALLFLCLALIMKILP 390
DB 363 GFETCHARPLGOSQVLSLSVHYKGLISTAFSNGAFGLIGITALLFLCLALIMKILP 422
QY 391 KERTOTETPRFPRSHSTILDVNVVPTAGPLAQKNOKATNSRTPPLPCAPSPESKK 450
DB 423 KERTOTETPRFPRSHSTILDVNVVPTAGPLAQKNOKATNSRTPPPPPAPSPESKK 482
QY 451 NOKKQYQLPSFPKSKSTQAPESQESQEBELHYATLNFPGVRPRPEARMKPGTQADYAEVK 510

DB 483 NOKKQYQLPSFPKSKSTQAPESQESQEBELHYATLNFPGVRPRPEARMKPGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544
RESULT 9
US-09-999-832A-259
; Sequence 259, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1063
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-04-27

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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 9; Length 544;

Best Local Similarity 74.8%; Pred. No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

Qy 1 MLAPLLLSLLGGSQAMDGRFWIRVOESVMVPEGLCISVPCSFSPROQDTGSTPAYGW 60

Db 1 MLAPLLLSLLGGSQAMDGRFWIRVOESVMVPEGLCISVPCSFSPROQDTGSTPAYGW 60

Qy 61 FKAVTETTKGAPVATNHQREVEMSTRGRPQLTGDPKNCNSLVIRDAQKQDESYFFRV 120

Db 61 FAVVETTKGAPVATNHOQREVEMSTRGRFQITGPAKNGSLVIRDAQMDESQYFFRV 120
QY 121 ERGSYRYNFMNDGFFLKVTALTQKPDVYIPETLEFGQPVTVICVENWAFEECPPPSW 180
Db 121 ERGSYTYNFMNDGFFLKVT----- 140
QY 181 TGAALSSQGTKTTSHFSVLSTPPODHTDLTCHVDFSRKGVSAQRTVLRVAYAPRD 240
Db 141 -----VLSTPPODHTDLTCHVDFSRKGVSAQRTVLRVAYAPRD 182
QY 241 LVISIRSDNTTP----- 252
Db 183 LVISIRSDNTPALEFQPOGNVPYLEAQKQFURLLLCAADSOPTATLSWLNQRLVSSHP 242
QY 253 -----PPENLRVMVSOANRTVLE 270
Db 243 WGPRLUGLPGVYAGDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLE 302
QY 271 NLNGTSLFVLBGQSILCLVCVTHSSPPARLSTQRGQVLSPOQSDPGVLELPRVQVSEH 330
Db 303 NLNGTSLFVLBGQSILCLVCVTHSSPPARLSTQRGQVLSPOQSDPGVLELPRVQVSEH 362
QY 331 GBFTCHARPLGSOHVLSLSVHYKKGLISTAFSNGAFIGITALLFLCLALIMKILP 390
Db 363 GBFTCHARPLGSOHVLSLSVHYKKGLISTAFSNGAFIGITALLFLCLALIMKILP 422
QY 391 KRTOTETPRFRSHSTILDVNVPTAGPLAQKRNOKATENSRTPLPGCAPSPESKK 450
Db 423 KRTOTETPRFRSHSTILDVNVPTAGPLAQKRNOKATENSRTPLPGCAPSPESKK 482
QY 451 NQKQVQLPSPFPKPSSTQAPESQSBELHYATLNFQGVRRPRPRMPKGTQADYAEVK 510
Db 483 NQKQVQLPSPFPKPSSTQAPESQSBELHYATLNFQGVRRPRPRMPKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 10

US-09-978-189-259
; Sequence 259, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

Qy 1 MLLPLLLSSLLGSSQAMDGFWIRVOESVMPVGLCLISVPCSFSPQDWTGSTPAYGYW 60
Db 1 MLLPLLLSSLLGSSQAMDGFWIRVOESVMPVGLCLISVPCSFSPQDWTGSTPAYGYW 60
Qy 61 FKAVTETTKGAPVATNHSREVEVSTGRFQLTGDPAKGNCSLVIRDAQMDSQYFFRV 120
Db 61 FKAVTETTKGAPVATNHSREVEVSTGRFQLTGDPAKGNCSLVIRDAQMDSQYFFRV 120
Qy 121 ERGSYVYVNFMDGFFKVLTALTQKPDVYIPEILEPQPTVVICVFNWAFEECPSPFSW 180
Db 121 ERGSYVYVNFMDGFFKVLTALTQKPDVYIPEILEPQPTVVICVFNWAFEECPSPFSW 180
Qy 181 TGAALSSQGTKP*TSHPFVLSFTPRPODHDITDCHVDFSRKGVSAQRTVRLRVAVAPRD 240
Db 141 -----VLSFTPRPODHDITDCHVDFSRKGVSAQRTVRLRVAVAPRD 182
Qy 241 LVISIRDNTPD----- 252
Db 183 LVISIRDNTPALEPQPGNVPLYEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSH 242
Qy 253 -----PPENLRVMVSOANRTVLE 270
Db 243 WGPRLGLELPVGVKAGDSGRYTCRAENRLSQOQALDLSVQYPPENLRVMVSOANRTVLE 302
Qy 271 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQGOVLSPPSQSPDGVLELPRVQVEHE 330
Db 303 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQGOVLSPPSQSPDGVLELPRVQVEHE 362
Qy 331 GEFTCHARHPLGSHVSLSLSVHYKGLISTAFNSGAFLGIGITALLFLCLALIMKILP 390
Db 363 GEFTCHARHPLGSHVSLSLSVHYKGLISTAFNSGAFLGIGITALLFLCLALIMKILP 422
Qy 391 KRTQTETPRFRSRHSTILDYINNVPTAGLAKQBNQKATNSPRTPLPFGAPSPESKK 450
Db 423 KRTQTETPRFRSRHSTILDYINNVPTAGLAKQBNQKATNSPRTPLPFGAPSPESKK 482
Qy 451 NQKQYQLPSFPFPKSTQAPESQSEELHYATLNFPGVYRPPRPEARMKGTQADYAEVK 510
Db 483 NQKQYQLPSFPFPKSTQAPESQSEELHYATLNFPGVYRPPRPEARMKGTQADYAEVK 542
Qy 511 FQ 512
Db 543 FQ 544

RESULT 11
US-09-978-608A-259
; Sequence 259, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 259
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-259

Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSLGSGQAMDRFWIRVQESVMVPEGLCISVPCSFSPRQDWTGSTPAYGYW 60
DB 1 MLPLLLSLGSGQAMDRFWIRVQESVMVPEGLCISVPCSFSPRQDWTGSTPAYGYW 60

QY 61 FRAVETTTGAPVATNHQREVMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
DB 61 FRAVETTTGAPVATNHQREVMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120

QY 121 ERGSYRYNFMMDGFFLKVTALTKQPDVYIPTELEBQPVVICVFNWAFBECPPPSFW 180
DB 121 ERGSYRYNFMMDGFFLKVT-----VLSFTPRPDNDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182

QY 181 TGAALSSQGTKPTTSFHSVLSTPRPDNDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
DB 141 -----VLSFTPRPDNDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182

QY 241 LVISISRDNTPD----- 252
DB 183 LVISISRDNTPALEPQPGNVPLYEAQKGFLLCAADSQPPATLSWVLQNRVLSSHP 242

QY 253 -----PPENLRVMVSCANRTVLE 270
DB 243 WGPRLGLELPGVKAGDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSCANRTVLE 302

QY 271 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTORQVLSPPSQSPDPGVLELPRVOVEHE 330
DB 303 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTORQVLSPPSQSPDPGVLELPRVOVEHE 362
QY 331 GEFTCHARPLGSHVSLSVHYKGLISTAFSNGAFJGIGITALLFLCLALIIIMKILP 390
DB 363 GEFTCHARPLGSHVSLSVHYKGLISTAFSNGAFJGIGITALLFLCLALIIIMKILP 422
QY 391 KRTOETPRPRFSRSTILDYINVVPTAGLAKNQKATPNSPRTPLPPGAPSPESKK 450
DB 423 KRTOETPRPRFSRSTILDYINVVPTAGLAKNQKATPNSPRTPLPPGAPSPESKK 482
QY 451 NQKKYQLPSPFPKSTQAPESQSEELHYATLNPFGVVRPEARMPKGTQADYAEVK 510
DB 483 NQKKYQLPSPFPKSTQAPESQSEELHYATLNPFGVVRPEARMPKGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

RESULT 12
US-09-978-585A-259
; Sequence 259, Application US/09978585A
; Publication No. US2003004963JA1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 259
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-259

Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSLGSGQAMDRFWIRVQESVMVPEGLCISVPCSFSPRQDWTGSTPAYGYW 60
DB 1 MLPLLLSLGSGQAMDRFWIRVQESVMVPEGLCISVPCSFSPRQDWTGSTPAYGYW 60

QY	61	FXAVTETTKGAPVATNHQSRVEMSTRGRQLTGDPAKGNCSLVIRDAQWQDESQYPRV	120
DB	61	FXAVTETTKGAPVATNHQSRVEMSTRGRQLTGDPAKGNCSLVIRDAQWQDESQYPRV	120
QY	121	ERGSVVRNFNMNDGFFLKVTALTQKPDVYIPETLEPCQPVVICVFNWAFECPEPSSW	180
DB	121	ERGSVVRNFNMNDGFFLKVT-----	140
QY	181	TGAALSSQGTXTTSHFSVLSTFPRPDHDTLTCHVDFSRKGVSAQRTVLRVAYAPRD	240
DB	141	-----VLSTFPRPDHNTDLTCHVDFSRKGVSAQRTVLRVAYAPRD	182
QY	241	LVISIRONTPD-----	252
DB	183	LVISIRONTFALBPQOGNVPLYEAKGQFLRLCCAOSQBPATLSWVLQNRVLSSHP	242
QY	253	-----PPENLRVWVQANRTVLE	270
DB	243	WGPRPLGLELPGVKAGDSGRVTCBAENLGSQQEALDLSVOQPPENLRVWVQANRTVLE	302
QY	271	NLNGNTSLPVLEGOSLCLVCVTHSSPPARLSWTQRQGVLSPSQSPDQVLELPRVQVBHE	330
DB	303	NLNGNTSLPVLEGOSLCLVCVTHSSPPARLSWTQRQGVLSPSQSPDQVLELPRVQVBHE	362
QY	331	GEFTCHABHPLGSOHVLSLSLVHVKGLISTASNGAFJGIGTALLFCLALIMKLIP	390
DB	363	GEFTCHABHPLGSOHVLSLSLVHVKGLISTASNGAFJGIGTALLFCLALIMKLIP	422
QY	391	KERTQTEPRPRFSRHSTILDYINVVPTAGPLAQKNQKATPNSRPTPLPPGAPSPESKK	450
DB	423	KERTQTEPRPRFSRHSTILDYINVVPTAGPLAQKNQKATPNSRPTPLPPGAPSPESKK	482
QY	451	NOKKOYOLPSPEPKSSTQAPESQESSEELHYATLNFPGVRRPRPEARMKGTQADYAEVK	510
DB	483	NOKKOYOLPSPEPKSSTQAPESQESSEELHYATLNFPGVRRPRPEARMKGTQADYAEVK	542

RESULT 13
US-09-978-191A-259
, Sequence 259, Application US/09978191A
, Publication No. US20030050239A1

APPLICANT: Askenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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APPLICANT: Filvaroff, Ellen
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; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 10; Length 544;

Best Local Similarity 74.8%; Pred.No. 4.6e-155;

Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLLPLLSSLLGGQAMDRFWIRVQESVMVPEGLCLISVPCSFSPYQDWTGSTPAYGYW 60
DB 1 MLLPLLSSLLGGQAMDRFWIRVQESVMVPEGLCLISVPCSFSPYQDWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNHQSRREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFVR 120
DB 61 FKAVTETTKGAPVATNHQSRREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFVR 120
QY 121 ERGSYVYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVCVFNWAFEECCPPFSW 180
DB 121 ERGSYVYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVCVFNWAFEECCPPFSW 180
QY 181 TGAALSQGTPTTSHPSVLSFTPRPDQHDIDLTCVDFSRKGVSAQRTVRLRVAYAPRD 240
DB 141 -----VLSFTPRPDQHDIDLTCVDFSRKGVSAQRTVRLRVAYAPRD 182
QY 241 LVISISRDNTPD----- 252
DB 183 LVISISRDNTPALPEFPQGNVPYLEAQGFRLLLCAADSQPPFATLSWVLQNRVLSSSH 242
QY 253 -----PPENLRVMVSOANRTVLE 270
DB 243 WGRPLGLELPGVKAGDSGRYTCAENRLSGOQALDLSVQYPPENLRVMVSOANRTVLE 302
QY 271 NLNGTSLPVLGGQSLCLVCVTHSSPPARLSWTQRGVLSQPSQPSDFGVLELPRVQVEHE 330
DB 303 NLNGTSLPVLGGQSLCLVCVTHSSPPARLSWTQRGVLSQPSQPSDFGVLELPRVQVEHE 362
QY 331 GEFTCHARHPLGSOHVSLSVHYKGLISTAFSNGAFLGIGITALLFLCLALLIMKILP 390
DB 363 GEFTCHARHPLGSOHVSLSVHYKGLISTAFSNGAFLGIGITALLFLCLALLIMKILP 422
QY 391 KRTQTETPRPRFSRHSHTILDYINVVFTAGFLAQKRNQKATPNSPRTPLPPGAPSPESKK 450
DB 423 KRTQTETPRPRFSRHSHTILDYINVVFTAGFLAQKRNQKATPNSPRTPLPPGAPSPESKK 482
QY 451 NQKQYQLPSPPEPKSSTQAPESQSEELHYATLNFPGVRPREARMKPGTQADYAEVK 510
DB 483 NQKQYQLPSPPEPKSSTQAPESQSEELHYATLNFPGVRPREARMKPGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

RESULT 14

US-09-978-403A-259
Sequence 259, Application US/09978403A

Publication No. US20030050240A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/518585
PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred.No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 149; Gaps 2;

Qy 1 MLPLLLSLGSGQAMDCRFWRVOCESVMVPEGLCISVPCSFSPYPRQDWTGSTAYGYW 60
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Qy 61 FRAVTEITKGPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
Db 61 FRAVTEITKGPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120

Qy 121 ERGSYVRYNFMNDGFLKVTALTKQEDVYIPETLEPGQPVTVCVFNWAFEECPFPSPRS 180
Db 121 ERGSYVRYNFMNDGFLKVTALTKQEDVYIPETLEPGQPVTVCVFNWAFEECPFPSPRS 180

Db 121 ERGSYVRYNFMNDGFLKVT----- 140
Qy 181 TGAALSSQGIKPTTSHFSVLSFTPRPODHTDLTCHVDFSRKGVSAORTVRLRVAYAPRD 240
Db 141 -----VLSFTPRPODHTDLTCHVDFSRKGVSAORTVRLRVAYAPRD 182
Qy 241 LVISISRDNTPD----- 252
Db 183 LVISISRDNTPALBPQGNVPYLEAQGOFLRLCAADSQPPATLSWVLQNRVLSSSH 242
Qy 253 -----PPENLRVMVSOANRTVLE 270
Db 243 WGRPLGLELPGVKAGDSGRYTCAENRLGSOQRALDLSVOYPPENLRVMVSOANRTVLE 302
Qy 271 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTQRGOVLSPSQSPDSFGVLELPRVQVEHE 330
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Qy 331 GEFTCHARHPLGSOHVSLSVHYKGLISTAFSNGAFLGIGITALLFLCLALIMKILP 390
Db 363 GEFTCHARHPLGSOHVSLSVHYKGLISTAFSNGAFLGIGITALLFLCLALIMKILP 422
Qy 391 KRRTOTETPRFRSHSTILDYINNVPTAGTACKRNOKATPNSPRTPLPPGAPSPESKK 450
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Qy 451 NQKQYQLPSPFPKSTQAPESQOEELHYATLNPFGVRPRPEARMKGTQADYAEVK 510
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Db 543 FQ 544

RESULT 15
US-09-978-564A-259
; Sequence 259, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottlieb, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585


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; PRIOR APPLICATION NUMBER: 60/085697

Query Match      83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 4,6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY      1 MLLPILLSLLGSGQAMDCGRFIRVQESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
DB      1 MLLPILLSLLGSGQAMDCGRFIRVQESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60

QY      61 FXAVTETTKGAPVATNHQREVMSTGRFQLTGDPKNCNCSLVIRDAQMDQESQYFFRV 120
DB      61 FXAVTETTKGAPVATNHQREVMSTGRFQLTGDPKNCNCSLVIRDAQMDQESQYFFRV 120

QY      121 ERGSVYVNFMDGFLKVTALTQKPDVYIPETLBPQGVTVICVFNWAFBECPPSPSW 180
DB      121 ERGSVYVNFMDGFLKVT----- 140

QY      181 TGAALSSQGTKEFTSHFSVLSFTPRPDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
DB      141 -----VLSTPRPDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182

QY      241 LVISISRDNTPD----- 252
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QY      253 -----PPENLRVMVSOANRTVLE 270
DB      243 WGRPLGLLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVSOANRTVLE 302

QY      271 NLNGTSLPVLGQSCLVCVTHSSPPARLSWTORGQVLSQSPSDPGVLELPRVQVEHE 330
DB      303 NLNGTSLPVLGQSCLVCVTHSSPPARLSWTORGQVLSQSPSDPGVLELPRVQVEHE 362

QY      331 GEFTCHARPLGSOHVLSLSVHYKKGLISTAFSGARLIGITALLFLCLALIIMKILP 390
DB      363 GEFTCHARPLGSOHVLSLSVHYKKGLISTAFSGARLIGITALLFLCLALIIMKILP 422

QY      391 KRRTQETPRPRFSRHSHTILDYINVVPTAGPLAQKNQKATNSPRTPLPPGAPSPESKK 450
DB      423 KRRTQETPRPRFSRHSHTILDYINVVPTAGPLAQKNQKATNSPRTPLPPGAPSPESKK 482

QY      451 NCKKQVQLSPFPKPSSTOAPESQESQELHYATLNFPGVRRPRBARMKGTQADYAEVK 510
DB      483 NCKKQVQLSPFPKPSSTOAPESQESQELHYATLNFPGVRRPRBARMKGTQADYAEVK 542

QY      511 FQ 512
DB      543 FQ 544
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Search completed: November 5, 2004, 14:13:46
Job time : 92.0765 secs

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GenCore version 5.1.6
Copyright (C) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 17.7654 Seconds
(without alignments)
3460.797 Million cell updates/sec

Title: US-09-937-636-4

Perfect score: 3377

Sequence: 1 MLLPILLSLIGSQAMDGR.....RPEARMKGTQADYAEVKFQ 639

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	487	14.4	626	A61084	myelin-associated
2	479	14.2	626	BNRT3	myelin-associated
3	469.5	13.9	582	BNRT3S	myelin-associated
4	466.5	13.8	637	B33785	myelin-associated
5	451.5	13.4	364	A30521	myeloid cell surfa
6	392	11.6	620	JH0593	Schwann cell myeli
7	368	10.9	403	I52590	m33-B isoform - mo
8	311	9.2	862	I43583	differentiation an
9	305.5	9.0	868	A45112	CD22 homolog/B lym
10	289.5	8.6	847	JH0371	B-cell adhesion pr
11	282.5	8.4	1694	S50065	sialoadhesin - mou
12	295	7.6	4391	A38096	perlecan precursor
13	251.5	7.4	628	I38000	Lutheran blood gro
14	245	7.3	647	A35648	B-cell adhesion pr
15	239.5	7.1	588	I37202	B-CAM protein - hu
16	236.5	7.0	761	IJHUNG	neural cell adhesi
17	235	7.0	725	IJRTNC	neural cell adhesi
18	235	7.0	858	IJMSNL	neural cell adhesi
19	235	7.0	1115	A32164	biliary glycoprote
20	231.5	6.9	526	I20992	hypothetical prote
21	226.5	6.7	575	T43290	hemictin precurs
22	226.5	6.7	598	I48950	telencephalin prec
23	226	6.7	917	S18252	heparan sulfate pr
24	226	6.7	3707	I241	nephlin - human
25	225	6.7	1241	T37190	nephlin cell adhesi
26	224	6.6	853	IJBONC	fasciclin II, tran
27	223.5	6.6	811	A41054	fasciclin II PI-li
28	223.5	6.6	873	B41054	fasciclin cell adhesi
29	218.5	6.5	1091	IJCHN4	neural cell adhesi

30 214 6.3 1040 2 A49356 transient axonal g
31 211 6.2 1040 2 A34695 axonal glycoprotei
32 210 6.2 1070 2 JC4593 protein-tyrosine k
33 206 6.1 464 2 C30127 transmembrane carc
34 204.5 6.1 538 2 JC3457 vascular cell adhe
35 203 6.0 462 2 T45633 connectin/titin -
36 201.5 6.0 458 2 JC1509 biliary glycoprote
37 201 6.0 1323 2 PNO568 connectin 3B - chi
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39 200.5 5.9 702 2 A36319 carcinoembryonic a
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42 197 5.8 435 2 D33258 pregnancy-specific
43 197 5.8 898 2 A40114 fasciclin II precu
44 196 5.8 1092 1 JN0635 neural cell adhesi
45 195.5 5.8 1209 2 T42718 probable neural ce

ALIGNMENTS

RESULT 1

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myelin-associated glycoprotein precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: A61084; A33263; PC2011
R:Spagnol, G.; Williams, M.; Srinivasan, J.; Golier, J.; Bauer, D.; Lebo, R.V.; Latov, N.
J. Neurosci. Res. 24, 137-142, 1989
A:Title: Molecular cloning of human myelin-associated glycoprotein.
A:Reference number: A61084; MUID:90064604; PMID:2479762
A:Accession: A61084
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-626 <SPA>
A:Cross-references: UNIPROT:P20916
R:Sato, S.; Fujita, N.; Kurihara, T.; Kuwano, R.; Sakimura, K.; Takahashi, Y.; Miyatake, Biochem. Biophys. Res. Commun. 163, 1473-1480, 1989
A:Title: cDNA cloning and amino acid sequence for human myelin-associated glycoprotein.
A:Reference number: A33263; MUID:89392083; PMID:2476987
A:Accession: A33263
A:Molecule type: mRNA
A:Residues: 1-613, 'T', 615-626 <SAT>
A:Cross-references: GB:M2973; NID:G187292; PIDN:AA59545.1; PID:G307156
R:Burger, D.; Pidoux, I.; Steck, A.J.
Biochem. Biophys. Res. Commun. 197, 457-464, 1993
A:Title: Identification of the glycosylated sequons of human myelin-associated glycoprotein
A:Reference number: PC2011; MUID:94092116; PMID:7505568
A:Accession: PC2011
A:Molecule type: protein
A:Residues: 84-98, 'X', 100-110; 210-222, 'X', 224; 245, 'X', 247-253; 309-318, 'XXX', 396-405, 'X', 4
C:Comment: This protein is a neural cell adhesion molecule.
C:Genetics:
A:Gene: GDB:MAG; GMA
A:Cross-references: GDB:I20702; OMIM:159460
A:Map position: 19q13.1-19q13.1
C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C:Keywords: brain; cell adhesion; glycoprotein; phosphoprotein; transmembrane protein
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F:20-626/Product: myelin-associated glycoprotein #status predicted <MAT>
F:35-102/Domain: immunoglobulin homology <IMM>
F:118-120/Region: cell attachment (R-G-D) motif
F:514-536/Domain: transmembrane #status predicted <TM>
F:99, 223, 246, 315, 406, 450, 454/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:106/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:334/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:543, 607/Binding site: phosphate (Thr) (covalent) #status predicted
F:573/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 14.4% ; Score 487; DB 1; Length 626;
Best Local Similarity 23.9% ; Pred. No. 2,4e-24;
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21 FWIRVQ-----ESVMVPEGLCLISVPCSFYPRQDWTGSTPAYGVFKAVTETT 68
10 FWMISASRGCHGWAMWPSISAFEGTCVSPICRPFDP--DELPAVAVHGVWVFNFSPEYK 67
69 KGAPVATNHOSREVMSTRGRFOLTDPAKGNCSLVIRDAQMDQESQYFPRVERGSYVRY 128
68 NYPPVVFVKSTQVHESFQGRSLLGLDGLRNCITLLSNVSPGLGKYFPRGDLGYNQY 127
129 NFM----- 131
128 TFSEHSVLDIVNTPNIVPPEVVAGTEVEVSCMVPNCPELPELSWLGHEGLGEPVLV 187
132 ---NDGFFLKVTLSFTREPQDHTDLTCHVDPSRKGVSQRTVPLRVAYAPRODLVISI 187
188 LRDEDEGTWQVSLHFPVTPREANGRLGCGQASFPNTTQFEGYASMDVKYPP--VIVEM 245
188 SRDNTPALEPQPGNVFYLEAQGFRLILCAADSOPTATLSWLNQNRVLSSSHMPGRPP 247
246 NSS-----VZAEIGSHVSLCGADSNPPPLLTWMDGTVLREA---VAES 287
248 LGLELPGVKAGDSGRVTCRAENPLGSCQALDLSVOYPPENLRVWVSQANRTVLENLNG 307
288 LLELEBEVTPAEDGVVACLAENAYGQDNRTVGLSVWYAPWKTIV-----NG 333
308 TSLPVLGEGSLCLVCVTHSPPARLSWTQRGQVLSQSPSDPGVLELPRVQVHEGEFTC 367
334 TWAV-EGEVSILCTQSNPDILTIFKEQILSVIYVESLQLELPAVSPEDDGEYWC 392
368 HARHPLGSHVLSVLSVHYSPKLLGPS-CSWABGLHSCSSQAQAPSLRWLWGEELLE 426
393 VAENQYQZATAPNLSEVAFVPLVLESRCAAARDTQCCLCVVKSNPSPVAPFELPSRNT 452
427 GNSQSDSEFTVPSSAGPWNSSLHGLSSGLRLCEANVHGAQSGSILQLPDKKGLI 486
453 VNSEREF-VYSERGLVITSLILRGQAQAPRVCTARNYGAKS---LELP----- 502
487 STAFSNG-----AFLGIGITALLFLCLAIIMKLPKRTQBTETPRPFRSHSTILDYIN 541
503 ---FOGAHRLMWAIGFVGAFAFALLIAIVCVITQTRKKNVTSPPSPS----- 549
542 VVETAGPLAKRQXATPNSPRTPLP-----GAPSP-ESKQXQKQYQLPSPPE 590
550 -----AGDN-----PVLFSDFRISGAPEKYESERRIGSERLLGL-- 586
591 PKSTQAPESQSBELHVALTNFPQPRPBARMPKGTQADYAEVK 637
587 -----RGEPPELDLSYHSDL-GKRTTKDSYTLSELAEYAEIR 624
RESULT 2
BNRT3
myelin-associated glycoprotein precursor, long splice form - rat
N:Alternate names: 1B236; brain neuron cytoplasmic protein 3; MAG
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Feb-1984 #sequence revision 31-Dec-1989 #text change 09-Jul-2004
C:Accession: A29028; A94175; A27185; A90836; I56564; A03138; A26362
R:Jai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Milner, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
A:Title: Two forms of 1B236/myelin-associated glycoprotein, a cell adhesion molecule for
A:Reference number: A29028; MUID:87232001; PMID:2433699
A:Accession: A29028
A:Molecule type: mRNA
A:Residues: 1-626 <LAI>
A:Cross-references: UNIPROT:P07722; GB:M16800; NID:G205269; PID:AAA1557.1; PID:G205270
R:Arquint, M.; Roder, J.; Chia, L.S.; Down, J.; Wilkinson, D.; Bayley, H.; Braun, P.; Du
Proc. Natl. Acad. Sci. U.S.A. 84, 600-604, 1987
A:Title: Molecular cloning and primary structure of myelin-associated glycoprotein.
A:Reference number: A94175; MUID:87092455; PMID:2432614
A:Accession: A94175
A:Molecule type: mRNA
A:Residues: 1-626 <ARQ>
A:Cross-references: GB:M14871; NID:G205267; PID:AAA41556.1; PID:G205268
R:Salzer, J.L.; Holmes, W.P.; Colman, D.R.

J. Cell Biol. 104, 957-965, 1987
A:Title: The amino acid sequences of the myelin-associated glycoproteins: homology to the
A:Reference number: A27185; MUID:87166195; PMID:2435742
A:Accession: A27185
A:Molecule type: mRNA
A:Residues: 1-626 <SAL>
A:Cross-references: GB:X05301; NID:G56611; PID:CAA28920.1; PID:G56612
R:Sutcliffe, J.G.; Milner, R.J.; Shimnick, T.M.; Bloom, F.E.
Cell 33, 671-682, 1983
A:Title: Identifying the protein products of brain-specific genes with antibodies to cDNA
A:Reference number: A90836; MUID:83259254; PMID:6347394
A:Accession: A90836
A:Molecule type: mRNA
A:Residues: 'KS', 311-626 <SUT>
A:Cross-references: GB:V01544; GB:J00756; NID:G56879; PID:CAA24786.1; PID:G818027
A:Experimental source: clone p1B236
A:Note: The authors translated the codon CAG for residue 350 as Asn
R:Bloom, F.E.; Battenberg, E.L.F.; Milner, R.J.; Sutcliffe, J.G.
J. Neurosci. 5, 1781-1802, 1985
A:Title: Immunocytochemical mapping of 1B236, a brain-specific neuronal polypeptide deduc
A:Reference number: I56564; MUID:85263773; PMID:4020419
A:Accession: I56564
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'KS', 311-626 <RES>
A:Cross-references: GB:M36702; NID:G203181; PID:AAA40831.1; PID:G203182
R:Sutcliffe, J.G.; Milner, R.J.; Bloom, F.E.
Cold Spring Harb. Symp. Quant. Biol. 48, 477-484, 1983
A:Title: Cellular localization and function of the proteins encoded by brain-specific MR
A:Reference number: I52892; MUID:84206577; PMID:6586369
A:Accession: I52892
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'KS', 311-626 <RE2>
A:Cross-references: GB:M11721; NID:G206780; PID:AAA42082.1; PID:G206781
C:Comment: The sequence contains five presumably extracellular domains that are distantly
C:Comment: The long form predominates in early postnatal life; alternative splicing prod
C:Comment: The papers cited variously predict the mature protein to begin at residue 19.
C:Genetics:
A:Gene: MAG
A:Map position: 7
C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C:Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; transcript
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-626/Product: myelin-associated glycoprotein, long splice form #status predicted <MA
F:35-102/Domain: immunoglobulin homology <IMM1>
F:118-120/Region: cell attachment (R-G-D) motif
F:152-219/Domain: immunoglobulin homology <IMM2>
F:254-307/Domain: immunoglobulin homology <IMM3>
F:340-394/Domain: immunoglobulin homology <IMM4>
F:425-490/Domain: immunoglobulin homology <IMM5>
F:514-536/Domain: transmembrane #status predicted <TM>
F:537-626/Domain: intracellular #status predicted <INT>
F:99, 223, 246, 315, 332, 406, 450, 454/Binding site: carbohydrate (Asn) (covalent) #status pred
Query Match 14.2%; Score 479; DB 1; Length 626;
Best Local Similarity 23.6%; Pred. No. 7.9e-24;
Matches 166; Conservative 104; Mismatches 260; Indels 172; Gaps 19;
Qy 21 FWIRVQ-----ESVMVPEGLCLISVPCSFYPRQDWTGSTPAYGVFKAVTETT 68
Db 10 FWMISASRGCHGWAMWPSISAFEGTCVSPICRPFDP--DELPAVAVHGVWVFNFSPEYK 67
Qy 69 KGAPVATNHOSREVMSTRGRFOLTDPAKGNCSLVIRDAQMDQESQYFPRVERGSYVRY 128
Db 68 NYPPVVFVKSTQVHESFQGRSLLGLDGLRNCITLLSNVSPGLGKYFPRGDLGYNQY 127
Qy 129 NFM----- 131
Db 128 TFSEHSVLDIVNTPNIVPPEVVAGTEVEVSCMVPNCPELPELSWLGHEGLGEPVLV 187
Qy 132 ---NDGFFLKVTLSFTREPQDHTDLTCHVDPSRKGVSQRTVPLRVAYAPRODLVISI 187

Db 188 RLREDEGTWQVSLHLLHVPFTRANGHRLGCGAAPPNTTLQFEGYASLDVKYPP--VIVEM 245
QY 188 SRDNTPALEPQGNVPLEAKQGFLLCAADSQPAPATLSWLNQVLSHSPWGRPP 247
Db 246 NSS-----VEAIEGSHVSLLCGADSNPPPLLTWMDGMYLREA---VAES 287
QY 248 LGLELPGVKAGDSGRYTCRAENRLGSGQALDLSVQYPPENLRVNVMSQANRTVLENLNG 307
Db 288 LYLDEEVTPEADGIYACLAENAYGQDNRTVELSVWYAPWKPTV-----NG 333
QY 308 TSLPVLGQSLCLVCTHSSPPARLSWTQGVLSFSPQSDPGVLELPRVQVEHEGFTC 367
Db 334 TVAV-EGEVSILGSTOSNPPDILTIKFKQILATVYESQLQLELPAVTPDDGEYWC 392
QY 368 HARHPLGSHVLSLVHYSPKLLGPS-CSWEAEGHLHSCSSQASPAPSLRWLGEELLE 426
Db 393 VAENQYQGRATAFNLSVEFAPITLLESHCAARDTVQCLVKSNPPEFSAFELPSRNV 452
QY 427 GNSQDSFEVTPSSAGPWANSSLSHGLSSGLRLCRCEAWNVHGAQSGSILQLPDKKGLI 486
Db 453 VNETEREF-VYERSGGLLTSLTRGQAQAPPRVICTSRNLXGTQS---LPLP----- 502
QY 487 STAFSNG-----AFIGIGITALLFLCLALIIMKILPKERTQTETPRPSRHSITLDVIN 541
Db 503 ---FOGAHRLMWAKIGPVGAVFAILIAVCYITQTRKXNVTPSPSFS----- 549
QY 542 VVPTAGPLAQKNKATNSPRTPLPP-----GAPSP-ESKKNQKQYQLSPFPBPKSST 595
Db 550 ----AG-----DNPHVLSPEPRISGAPDKYSEKRLGSERRLLGL----- 586
QY 596 QAPESQESSEELHYATLNPFGVRPPEARMKGTQADVAEVK 637
Db 587 ---RGEPPDLDSYSHSDL-GKRPTKDSYTLTEELAEVAEIR 624

RESULT 3
ENR335
myelin-associated glycoprotein precursor, short splice form - rat
N:Alternate names: 1B236; brain neuron cytoplasmic protein 3; MAG
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text_change 16-Jun-2000
C:Accession: B29028; B27185; A60055
R:Lai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
A:Title: Two forms of 1B236/myelin-associated glycoprotein, a cell adhesion molecule for
A:Reference number: A29028; MUID:87232001; PMID:2438699
A:Accession: B29028
A:Molecule type: mRNA
A:Residues: 1-582 <LAI>
A:Cross-references: GB:M22357; NID:G205271; PIDN:AAA1558.1; PID:G205272
R:Salter, J.L.; Holmes, W.P.; Colman, D.R.
J. Cell Biol. 104, 957-965, 1987
A:Title: The amino acid sequences of the myelin-associated glycoproteins: homology to th
A:Reference number: A27185; MUID:87166195; PMID:2435742
A:Accession: B27185
A:Molecule type: mRNA
A:Residues: 419-582 <SAL>
A:Cross-references: GB:X06554; NID:G56614; PIDN:CAA29797.1; PID:G1334302
R:Tropak, M.B.; Johnson, P.W.; Dunn, R.J.; Roder, J.C.
Brain Res. Mol. Brain Res. 4, 143-155, 1988
A:Title: Differential splicing of MAG transcripts during CNS and PNS development.
A:Reference number: A60055
A:Accession: A60055
A:Molecule type: mRNA
A:Residues: 565-582 <TRO>
C:Comment: The sequence contains five presumably extracellular domains that are distantl
C:Comment: The short form is found in the adult; the long form predominates in early pos
C:Genetics:
A:Gene: MAG
A:Map position: 7
C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C:Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; trans
F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-582/Product: myelin-associated glycoprotein, short splice form #status predicted <M
F:35-102/Domain: immunoglobulin homology <IMM1>
F:118-120/Region: cell attachment (R-G-D) motif
F:152-219/Domain: immunoglobulin homology <IMM2>
F:254-307/Domain: immunoglobulin homology <IMM3>
F:340-394/Domain: immunoglobulin homology <IMM4>
F:425-490/Domain: immunoglobulin homology <IMM5>
F:514-536/Domain: transmembrane #status predicted <TM>
F:537-582/Domain: intracellular #status predicted <INT>
F:99, 223, 246, 315, 332, 406, 454/Binding site: carbohydrate (Asn) (covalent) #status prec

Query Match 13.9%; Score 469.5; DB 1; Length 582;
Best Local Similarity 24.7%; Pred. No. 36-23;
Matches 146; Conservative 89; Mismatches 226; Indels 129; Gaps 13;

QY 21 FWIRVQ-----ESWVMEGLICISVPSCFSFVPRODWTGSTPAYGVFKAVTETT 68
Db 10 FWIMISASRGHWGAMPSSISAFEGTCVSIKCFDFP--DELRPVAVHGVWFNSPYK 67
QY 69 KGAPVATNHQSREVMSRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRVERGSVRY 128
Db 68 NYPVWFKSRTOVVHESFQGRSRLLDGLGRNCTLLSTLSPELGGKYPRGLGGYNY 127
QY 129 NFM----- 131
Db 128 TFSEHSLDINTPNIVVPEVAGVEVSCVMPDNCPELRPELSWLGHEGEPVLG 187
QY 132 ---NDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPDLVISI 187
Db 188 RLREDEGTWQVSLHLLHVPFTRANGHRLGCGAAPPNTTLQFEGYASLDVKYPP--VIVEM 245
QY 188 SRDNTPALEPQGNVPLEAKQGFLLCAADSQPAPATLSWLNQVLSHSPWGRPP 247
Db 246 NSS-----VEAIEGSHVSLLCGADSNPPPLLTWMDGMYLREA---VAES 287
QY 248 LGLELPGVKAGDSGRYTCRAENRLGSGQALDLSVQYPPENLRVNVMSQANRTVLENLNG 307
Db 288 LYLDEEVTPEADGIYACLAENAYGQDNRTVELSVWYAPWKPTV-----NG 333
QY 308 TSLPVLGQSLCLVCTHSSPPARLSWTQGVLSFSPQSDPGVLELPRVQVEHEGFTC 367
Db 334 TVAV-EGEVSILGSTOSNPPDILTIKFKQILATVYESQLQLELPAVTPDDGEYWC 392
QY 368 HARHPLGSHVLSLVHYSPKLLGPS-CSWEAEGHLHSCSSQASPAPSLRWLGEELLE 426
Db 393 VAENQYQGRATAFNLSVEFAPITLLESHCAARDTVQCLVKSNPPEFSAFELPSRNV 452
QY 427 GNSQDSFEVTPSSAGPWANSSLSHGLSSGLRLCRCEAWNVHGAQSGSILQLPDKKGLI 486
Db 453 VNETEREF-VYERSGGLLTSLTRGQAQAPPRVICTSRNLXGTQS---LPLP----- 502
QY 487 STAFSNG-----AFIGIGITALLFLCLALIIMKILPKERTQTETPRPS 531
Db 503 ---FOGAHRLMWAKIGPVGAVFAILIAVCYITQTRKXNVTPSPSFS 549

RESULT 4
B33785
myelin-associated glycoprotein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 23-Jul-1999
C:Accession: B33785; A33785; S05687; S02374
R:Fujita, N.; Sato, S.; Kurihara, T.; Kuwano, R.; Sakimura, K.; Inuzuka, T.; Takahashi, I
Biochem. Biophys. Res. Commun. 165, 1162-1169, 1989
A:Title: cDNA cloning of mouse myelin-associated glycoprotein: a novel alternative splic
A:Reference number: A33785; MUID:90121220; PMID:2482022
A:Accession: B33785
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-637 <FUJ>
A:Cross-references: GB:M31811
A:Accession: A33785
A:Status: preliminary

J. Immunol. 141, 2797-2800, 1988
A:Title: Isolation of a cDNA encoding CD33, a differentiation antigen of myeloid progenitor cells
A:Reference number: A30521; MUID:89009814; PMID:3139766
A:Accession: A30521
A:Molecule type: mRNA
A:Residues: 1-364 <SIM>
A:Cross-references: UNIPROT:P20138
C:Genetics:
A:Gene: GDB:CD33
A:Cross-references: GDB:119762; OMIM:159590
A:Map position: 19q13.3-19q13.4
C:Keywords: glycoprotein; surface antigen; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-259/Domain: extracellular #status predicted <EXT>
F:260-282/Domain: transmembrane #status predicted <TM>
F:283-364/Domain: intracellular #status predicted <CYT>
F:100,113,160,209,230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.4%; Score 451.5; DB 2; Length 364;
Best Local Similarity 21.3%; Pred. No. 2.6e-22;
Matches 148; Conservative 49; Mismatches 110; Indels 389; Gaps 11;

QY 1 MLLPULLSSLLGGQAVMDGRFWRVQBSVMVPEGLCISVPCSFSPYRQDWTGTPAYGYW 60
DB 1 MPELLLLPALLMAGALAMDPNFWLQVQBSVTVQEGCLVLPCTFPHPIPYDYDKNSPVHGYW 60

QY 61 FKAVTETTKGAPVATNHQSREVENMSTGRFQLTGDPKAGNCSLVIRDAQMDQESQYFVRV 120
DB 61 FREGAIIISGSPVATNKLDOEVEETGRFRLGDPGRNNCSLSIVDARRRDNQSYFFRM 120

QY 121 ERGSYVAYNFMNDGFFLKVT 140
DB 121 ERGS-TKSYKSPQLSVHVDLTHRPKILIPGLTLEPGHSLNLTCSYSWACEQGTPPIFSW 179

QY 141 -----VLSFTPRPDHNTDLTCHVDPSRKGVAQRTVRLVAYAPRDLV 184
DB 180 LSAAPTSGLPRTTHSSVLIITPRPDHNTLTCQVPAGAGVTTERITQLNVTV 235

QY 185 ISISRDNTPALEPOGQNVFLEAQKQFLRLCAADSQPPATLSWVLQNRVLSHHPWG 244
DB 236 -----QNPTT----- 240

QY 245 PRPLGLELPVKAGD-SGRYTCRAENRLGQQRALDLSVQYPPENLRVMVSWANRVLEN 303
DB 241 -----GTFPGDGGKQETRA----- 255

QY 304 LGNCTSLPVLEGQSLCLVCTHSPPARLSMTORGQVLSFSPQSDPGVLELPRVQVEHEG 363
DB 256 -----GV----- 257

QY 364 EFTCHARHPLGSHVSLSVSHYSPKILGSPCSWEAEGHLCSSQASPAFLRWMLGEE 423
DB 258 ----- 257

QY 424 LLEGNSSQDSFEVTPPSAGPWANSSLSLHGGLSGLLRCEANVHCAQSGSILQPDKK 483
DB 258 -----VHGAIGGA----- 265

QY 484 GLISTAPNGAFLGIGITALLFLCLALIMKILPKRTQTETPRPRFSRHSITLDYINV 543
DB 266 -----GVALLALCLCLIFIVKTHRKAARTAVGRNDTH----- 300

QY 544 PTAGPLAKKNQKATNSPRTPLPGAPSPESKKNOKKQVLPSPFPKSKSTQAPESQES 603
DB 301 PTTGSASPKEQKSKLHGP-----TETSCSGAAPTVM 334

QY 604 QEELHVAATLNPVGRPEARMKPGTQADYAEVKFO 639
DB 335 DEELHVASLNFHGNP-----SKDTSTEYSEVTRTQ 364

Schwann cell myelin protein precursor - Japanese quail
C:Species: Coturnix coturnix japonica (Japanese quail)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: JH0593; PS0356
R:Dulac, C.; Tropak, M.B.; Cameron-Curry, P.; Rossier, J.; Marshak, D.R.; Roder, J.; Le
Neuron 8, 323-334, 1992
A:Title: Molecular characterization of the schwann cell myelin protein, SMP: structural
A:Reference number: JH0593; MUID:92153423; PMID:1739462
A:Accession: JH0593
A:Molecule type: mRNA
A:Residues: 1-620 <DUL>
A:Cross-references: UNIPROT:092154; GB:S83711; NID:G245729; PIDN:AAB21466.1; PID:G245730
A:Experimental source: spinal cord
A:Note: the species of quail is not identified
A:Accession: PS0356
A:Molecule type: protein
A:Residues: 18-31;119-132
C:Comment: This protein is expressed on all external membranes of Schwann cells.
C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-620/Product: Schwann cell myelin protein #status experimental <SCH>
F:33-101/Domain: immunoglobulin homology <IMM>
F:506-533/Domain: transmembrane #status predicted <TM>
F:222,314,331,405,449/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.6%; Score 392; DB 2; Length 620;
Best Local Similarity 23.5%; Pred. No. 48-18;
Matches 169; Conservative 89; Mismatches 270; Indels 192; Gaps 24;

QY 5 LLLSLGGSQAMDGFRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAY--GYWFK 62
DB 4 LVLTVLLMGTCISAPWAAWMPFMAALSGTCVQLPCRFDPYEE---LRPASIGGLWV- 58

QY 63 AVTETTKGAP-----VATHQREVMSTRGRFQLTGDPKAGNCSLVIRDAQMB- 113
DB 59 -----FGSPYKPNYPVVARSRPSAVHESFAGRASFLGDTGRDCTLNI--AELSEEL 110

QY 114 -SQYFRVRGSGVRYNF-----SFEHAEALDVAAPHLEVPHELVAAGSEAILCRVPCNPRLPL 170
DB 111 AGKYIFRGDLGGVNYQSFSEHAEALDVAAPHLEVPHELVAAGSEAILCRVPCNPRLPL 170

QY 131 -----MNDGFFLKTV--LSFTPRPDHNTDLTCHVDPSRKGVSQAQT 171
DB 171 LTWTGTELLDPTGKERIEDDLGSKSLGLSRLFRPRKEDLGRVCGVTFFINSLSFOAD 230

QY 172 VRLVAYAPRDLVISISRDNTALEPOPOGNVYPYLEAQKQFLRLCAADSOPTATLSWV 231
DB 231 VGLDVQY-----EPQVVLGMPTEVEGSDVELGCGRAEGRPAPLISWF 273

QY 232 LQNRVLSSSHPPGPRPLGLELPVKAGDSGRYTCRAENRLGSCQALDLSVOYPPENLRV 291
DB 274 RGSEVLRB---PGRNRLLLSNVGGDDGGSFSCVAENHGRHRSLSQLRVAYAP---RA 327

QY 292 MYSQANRTVLENLNGTSLPVLEGSLCLVYTHSSPPARLSWTOGQVLSQPSQSDPGV 351
DB 328 PVI-----NG-SLWVVGSDPVSVTCRAESEPAAILVLRGKVMMAAIVEDHVT 375

QY 352 LELPVRQVHEGEFTCHARHPLGQSQVLSLSVHYSPKLLGPS-CSWEAEGLHCSCSSQA 410
DB 376 MEMRPARPDGGTYSCVAENQHCASTSFNISVEYPLVLPASRCTAGDGVRCVMWNS 435

QY 411 SPAPSLRWLGBELLEGNSSQSFVTPSSAGFWANSSLSLHGGLSSGLRLRCEANVHVG 470
DB 436 IPDSSLVFEPLTRNQVSDGHRDFTAAPPGSDGSITGLTRGPLEPRLLVLCARNRHG 495

QY 471 AOGSGTILQPKKGLISTAFNSGAPFG-IGITALLFLCLALIMKILPKRRQTOTPRPR 529
DB 496 TTAQO-LRHHPCGLV-----WAKGVPVGAUVAFAIVAVCY----- 532

QY 530 FGRHSTILDYINVVPTAGLAQRNOKATFNSPRTPLP-----GAPSESKNQ----- 579
DB 533 -----LSQSRKKGAGSEVTPVQPMAGFGGDDPLDLRPPQVRMLR 573

QY 580 --KKQYQLPSPFPKSTQAPESQSEELHYATLFPFGVRPAPRPMKGTQADYAEVK 637
DB 574 GAMERWAL----GVKEGSGAP--QEVPTTSH-----PMKP---TRGPLEDPPEYAEIR 618

RESULT 7
152590
m33-B isoform - mouse
C:Species: Mus sp. (mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: 152590
R:Tchilian, E.Z.; Beverley, P.C.; Young, B.D.; Watt, S.M.
Blood 83, 3188-3198, 1994
A:Title: Molecular cloning of two isoforms of the murine homolog of the myeloid CD33 anti
A:Reference number: 152590; MUID:94250900; PMID:8193354
A:Accession: 152590
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-403 <RES>
A:Cross-references: GB:S71345; NID:G551352; PIDN:AAB30842.1; PID:G551353

Query Match 10.9%; Score 368; DB 2; Length 403;
Best Local Similarity 36.9%; Pred. No. 8.7e-17;
Matches 90; Conservative 22; Mismatches 72; Indels 60; Gaps 3;

QY 1 MLLPLLLSSLLGGSOAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
DB 1 MLWPLPLFLCAGSLAQDLFQLVAPESVTEEGLCVHVFCVSFYPSIKLT-LCPVTGSW 59

QY 61 FKAVTETTKGAPVATNHQSRREVMSTRGRFQLTGDPKAGNCSLVIRDAQMBQESQYFRV 120
DB 60 LRKGVSLHEDSPVATSDPRQLVQKATQGRFQLLGDQPKHDCSLFIRDAQKNDTGMYPFRV 119

QY 121 ERGSYVRYNFMNDGFFLKVT----- 140
DB 120 VREFVRYSYKKKSLSLHVTLSLSTPDIIPGLEAGYPNLTCSPWACEQGTPTPTFSW 179

QY 141 -----VLSTPRPDHNTDLTCHVDPSRKGVSQAQRTVRLRVAYAP---R 181
DB 180 MSTALTSLSSRTTDSVLITFTFPQDQHGKTLCTLVTSFGAGVTVERTIQLNVTKSGQMR 239

QY 182 DLVI 185
DB 240 ELVL 243

RESULT 8
149583
differentiation antigen - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 149583
R:Law, C.
J. Immunol. 151, 175-187, 1993
A:Title: Organization of the murine Cd22 locus. Mapping to chromosome 7 and characterizat
A:Reference number: 149583; MUID:9315834; PMID:8100843
A:Accession: 149583
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-862 <RES>
A:Cross-references: UNIPROT:P35329; GB:L16928; NID:G348965; PIDN:AAA02562.1; PID:G348966
C:Genetics:
A:Gene: CD22

Query Match 9.2%; Score 311; DB 2; Length 862;
Best Local Similarity 21.5%; Pred. No. 1.2e-12;
Matches 197; Conservative 97; Mismatches 276; Indels 346; Gaps 42;

QY 5 LLLSLGGSQAMDGFRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 61
DB 9 LLILGHAAASQYSSANDMTVDHPQTLFAWEGACIRIFCKYKTPLPFKARLNDILLFQNYEF 68

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QY 62 KAVTETTKGAPVATNHQSRREVMSRGRFOLTGDPKAGNCNSLVIRDAQMDQESQYFFRVE 121
DB 69 DKATKFKGT-VLYNKAEPFLYPPKORRTFLGN-SIDNCTLXIHIPRANSGNLGLRMT 126
QY 122 RGS-----YVR-----YN-----FMDGFLR 135
DB 127 AGTWRMEPIHLNVSEKPPQFYIQMPSEIRSESQSVTLTGLNPFSCFEYDILLQWLEDSK 186
QY 136 FLKVT-----VLSFTPRPDNDTLTCHVDYDFSRKGVSAQRTVRL 174
DB 187 ITSVTSEVTSITSSVTSIKNVVTSKLTQPKWTDHGSVKQVQHSSE-VLSERTVRL 245
QY 175 RVAYAP-----RDLVISISRDNT-----ALEPOQ 200
DB 246 DVKYTKLEIKVNPTEVEKNNSVTMTCRVNSNPKLRTVAWSFKDGRPLEQDELEQEQ 305
QY 201-----GNVPYLE-----AKQGFRLR 215
DB 306 MSKLIHLSVTKMGRKYRQCOASNDIGEGSEEEVELTVHYAPEFSRVHIYPSAEEGOSVE 365
QY 216 LLCAADSQPPAT-LSWVLQNRVLSSSHPPGPRFLGLELPGVAGDSGRYTCAENRLG-- 272
DB 366 LICESLASPSATYTWHRKPIP-----GDTQEKLRIPKVPFWHAGNYSCLAENRLHG 420
QY 273 --SQORALDSVQYPENLRVMVSOANRTVLENLNGTSLPVLGOSCLVCVTHSSPPA 330
DB 421 KIDQEKLD--VHYAP-----KAVTTVIOSF-----TPILEGDSVTLVCRVNSNPD 465
QY 331 RLS--WTQR--GOVLSQSPQSDPGVLELPRVQVEHEGFTCHARPLGSGHVSLSVHY 386
DB 466 VTSYRNWPOSGSVLK-----PGVLRIOKVTWD-SMPVSCAACNHCSCWALPVLNVHY 518
QY 387 SP---KLLGPS-----WEAEG----- 401
DB 519 APRDVKLVKVPASEIRAGORVLLQCDPAESNPAEVRFFWKNGSLVQGRYLSFGSVSP 578
QY 402-----LHSCSSQASAPSLRWL-----GELLEGNSSQDSFEVTPSSA 441
DB 579 EDGNYNCMVNNSIGTSLQAMWLQVLYAPRRLRVSISPGDHVMEGKATLSCE---SDA 635
QY 442 GP-----WANSS-LSLHGSLGSLRCEANVHGAQS-----GSILQLPDKKGL 485
DB 636 NPISQYTWFDSSQDLH---SSGQKLALEPLEVQHTGSYRCKGTNGIGTSSPSTLTIV 692
QY 486 ISTAFNGAPLGTITALLFLC-LALIIMKILPK-----RRTOTETPRPSRHSHTILDYIN 541
DB 693 YVSPETIGKRVAGLGLFCLTICILAIWGMKIQKMKQNSQQGLQF----- 738
QY 542 VVPTAGPLAKRNOKATPNSRPTLPFGAPSPESK-----KNQKKQYOLPFPBP----- 591
DB 739 --NSSQOSFVRNKKAR---RTPLSEG---POSQCYNPAMDVTYSAILRFPESDMHN 789
QY 592-----KSSTQAPBSQS-----QELHYATLNFPGVRPRP 621
DB 790 AGDAGTAPATQAPPNNSDSVTSYVIQKRPMDGYENVNPNPCPEDESITHYSELVQFGAGKRP 849
QY 622 EARMKGTQADYAEVK 637
DB 850 QAK-----EDVDYVTLK 861

```

RESULT 9

A46512

CD22 homolog/B lymphocyte-restricted adhesion molecule - mouse

C1 Species: Mus musculus (house mouse)

C1 Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995

C1 Accession: A46512

R1 Species: Mus musculus (house mouse)

R1 Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995

R1 Accession: A46512

R1 Species: Mus musculus (house mouse)

R1 Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995

R1 Accession: A46512

R1 Species: Mus musculus (house mouse)

R1 Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995

R1 Accession: A46512

R1 Species: Mus musculus (house mouse)

R1 Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995

R1 Accession: A46512

A: Molecule type: nucleic acid
 A: Residues: 1-868 <TOR>
 A: Experimental source: B cell lymphoma 38C13
 A: Note: sequence extracted from NCBI Backbone (NCBI:116156)

Query Match 9.0%; Score 305.5; DB 2; Length 868;
 Best Local Similarity 21.3%; Pred. No. 2.9e-12;
 Matches 192; Conservative 92; Mismatches 251; Indels 365; Gaps 43;

```

QY 33 EGLCISVPCSF--YPRQDWTGSTPAYGVFKAVTETTKG-----APVATNHQSRREVMS 85
DB 38 EGACIRIPCKYKTPKARLDNILLFONYEDFKATKFTGTCLYNATKTEKDESELYLS 97
QY 86 TRGFQITGTPAKGNSLVIRDAQMDQESQYFFRVERGS-----YVR 127
DB 98 KQGRVTFGLNRI-DNCTLXIHIPRANSGNLGLRMTAGTWRMEPIHLNVSEKPPQFYIQ 156
QY 128-----YN-----FMDGFLKVT----- 140
DB 157 MPSEIRSQSVTLTGLNPFSCFEYDILLQWLEDSKTSITSSVTSIKNVYT 216
QY 141 --VLSFTPRPDNDTLTCHVDYDFSRKGVSAQRTVRLRVAYAP----- 180
DB 217 BSKLTQPKWTDHGSVKQVQHSSE-VLSECTVHLVDVKTPTKLEIKVNPTEVEKNNSVT 275
QY 181-----RDLVISISRDNT-----ALEPOQ----- 200
DB 276 MTCRVNSNPKLRTVAWSFKDGRPLEQDELEQEQQMSKLIHLSVTKMGRKYRQCOASND 335
QY 201 --GNVPYLE-----AKQGFRLLCALDASQPPAT-LSWVLQNRVLS 238
DB 336 IGPESEVELTVHYAPEFSRVHIYPSAEEGOSVELICESLASPSATYTWHRKPIP 395
QY 239 SSHPWGPRPLGLELPGVAGDSGRYTCAENRLG-----SQORALDSVQYPENLRVMS 294
DB 396 --GDTQEKLRIPKVPFWHAGNYSCLAENRLHGKIDQEKLD--VHYAP----- 440
QY 295 QANRTVLENLNGTSLPVLGOSCLVCVTHSSPPARLS--WTQR--GOVLSQSPQSDPG 350
DB 441 KAVTTVIOSF-----TPILEGDSVTLVCRVNSNPNVTSYRNWPOSGSVLK-----PG 489
QY 351 VLELPRVQVEHEGFTCHARPLGSGHVSLSVHYSP-----KLLGPS----- 394
DB 490 VLRIQKVTWD-SMPVSCAACNHCSCWALPVLNVHYAPRDVVKLVKVPASEIRAGORVLL 548
QY 395 -CS-----WEAEG-----LHSCSSQASAPSLRWL 420
DB 549 QCDPAESNPAEVRFFWKNGSLVQGRYLSFGSVSPEDSGNYNCMVNNSIGTSLQAMWL 608
QY 421-----GELLEGNSSQDSFEVTPSSAGP-----WANSS-LSLHGSLGSSG 458
DB 609 QVLYAPRRLRVSISPGDHVMEGKATLSCE---SDANPPIQYTWFDSSQDLH---SSG 662
QY 459 LRLCEAWNV-----HGAQS-----SILQLPDKKGLISTAFNGAPLGTIGI 500
DB 663 QKLALEPLEVQHTGSYRCKGTNGIGTGESPPSTLTIVYSPETIG-----KRVAGLGF 715
QY 501 TALLFLCLALIMKILPK---RRTOTETPRPSRHSHTILDYINVVPTAGPLAKRNOKA 557
DB 716 CLTIFI-LAIWGMKIQKMKQNSQQGLQF-----NSSQOSFVRNKKAR 758
QY 558 TPNSRPTLPFGAPSPESK-----KNQKKQYOLPFPBPESK-----STQAPESQE 602
DB 759 R---RTPLSEG---POSQCYNPAMDVTYSAILRFPESDMHNAGDAGTAPATQAPPNN 811
QY 603 S-----QELHYATLNFPGVRPRPEARMKGTQADYAEVK 637
DB 812 SDTVTSYVIQKRPMDGYENVNPNPCPEDESITHYSELVQFGAGKRPQAK-----EDVDYVTLK 867

```

RESULT 10

JH0371

B-cell adhesion protein CD22 beta splice form precursor - human

N:Alternate names: B-cell membrane protein CD22
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0371; 156171
R:Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
J. Exp. Med. 173, 137-146, 1991
A:Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell interaction
A:Reference number: JH0371; MUID:91086838; PMID:1985119
A:Accession: JH0371
A:Molecule type: mRNA
A:Residues: 1-847 <Will1>
A:Cross-references: UNIPROT:O60926; GB:X59350; NID:G36090; PIDN:CAA42006.1; PID:G36091
A:Experimental source: B lymphocyte
A:Note: the authors translated the codon AAT for residue 358 as Met
R:Wilson, G.L.; Naifeid, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.
J. Immunol. 150, 5013-5024, 1993
A:Title: Genomic structure and chromosomal mapping of the human CD22 gene.
A:Reference number: 156171; MUID:93267103; PMID:8496602
A:Accession: 156171
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 121-268, 'T', 271-473, 'K', 475-614, 'R', 616-638, 'Y', 640-711, 777-847 <WIL2>
A:Cross-references: GB:S61375; NID:G385980; PIDN:AAC18956.1; PID:G3184492
C:Genetics:
A:Gene: GDB:CD22
A:Cross-references: GDB:127545; OMIM:107266
A:Map position: 19q13.1-19q13.1
A:Intons: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-847/Product: B lymphocyte cell adhesion protein #status predicted <MAT>
F:346-398/Domain: immunoglobulin homology <IMM1>
F:609-661/Domain: immunoglobulin homology <IMM2>
F:688-705/Domain: transmembrane #status predicted <TRA>
F:67,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (covalent)
F:764,789/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 8.6%; Score 289.5; DB 2; Length 847;
Best Local Similarity 20.0%; Pred. No. 3.1e-11;
Matches 181; Conservative 116; Mismatches 278; Indels 331; Gaps 40;

QY 1 MLPLLLSLGSGQMDGRFWI-RVQSVVMVPEGLCTSVPCSPS-----YPRQ 48
DB 3 LLGPWLLLVLELAFSSSKKWFPHETLYAWEGACVMIPTYPALDGDLEPILFNP 62
QY 49 DWTGTPAYGWFKAIVETTKGAPYATNHSREVMSTRGRFQLTGDPAKNCSLVIRDA 108
DB 63 EYKNTSKFD--GTRLYESTKDGKVP-----SEQKRVQFLGDKNK-NTILSIHPV 109

QY 109 QMQDSQYFFRVER-----VTV-----LSFTPRPDHNTDLTCHV-DFSRKGV 166
DB 110 HLNDGQGLRLMESKTEKWMERIHNVSRPPPHIQLPPETQESQEVTLTCLLNFSCYG 169

QY 124 SVRYNFNDGFFLK-----VTV-----LSFTPRPDHNTDLTCHV-DFSRKGV 166
DB 170 YPIQLWLLGVPMQAAVTSLSIKSVFTSELSKFSQWGHGKIVTCQLQDADGKFL 229

QY 167 S-----AQTVRLEAVAPRDLVI-----POPOG-NVPYLEAQKQGL 214
DB 230 SNDTVQLNVKHTPKLEIKVTPSDAIVREGDSVTMTCEVSSSNPEYTVTSWLKDGSLKKQ 289

QY 191 NTPALE-----LQNRVLSLHHPWGRPRPLGLELPGVKAGDSGRYTCRAE 268
DB 290 NTFTLNLREVTKDQSGKYCCQVNSNDVGPGRSEVFLQVQYAFEPSTVQILHSPAVEGSOV 349

QY 215 RLLCAADSP-PATLSWV-----LQNRVLSLHHPWGRPRPLGLELPGVKAGDSGRYTCRAE 268
DB 350 EFLCNSLANPLTNYTHNGKEMQGRTEKH-----IPKILFWAGTVCVAE 399

QY 269 NPLGSOOR--ALDLSVQYPPENLRVWVSOANTVLENLNGTSLPVLGQSICLVCVTHS 326
DB 400 NILGTGQFGGAELDVOYPPKKV-----TTVIQN-----PMPIREGDTVTLSCNYS 446

QY 327 SPFA--RLSWTORGQVLSQSPSDPGVLELPRVQVHEGEFTCHARPLGSGHVSLSLV 384
DB 447 SNFSVTRYEWKPHGAEPEPSL-----GVLTQINQVNDNT-TIACARCNWSWASPVALNV 501

QY 385 HYSF-----KLLGSPSCSWEAEGLHSCSSQASPAFSLRWLGBELLGESSQDSFE- 435
DB 502 QYAPDRVRVRKIKPLSEIHSGNSVSLQCDPSS-SHPKEVQFFWEKNGRLLGKESQLNFD 560

QY 436 VTFSSAGP--WANSLS-----LHGLSSG-----LRLCEA-- 465
DB 561 ISPEDAGSYSCWYNSIGQTASKAWLTLEVLYAPRLRVSNPQDQVWEGKSATLTCESDA 620

QY 466 -----WN-----VHQAQSGSILQLPDKX-----GLIS-----TA 489
DB 621 NPPVSHYTWFDWNNQSLPHSQK--LRLEPVAVQHSYGAWCQGTNSVGKRGSPSLTLTV 677

QY 490 FSNAGFAGIGITALLFLCLALIMKI-----LPKR--RTQET-----PPRFS 531
DB 678 YSPETIGRRVAVGLGSLAILILAILCGLQSRWKTQSQGLQENSSQGSFFVRNKKV 737

QY 532 RHTSLDYINVPTAGTLAGKRNQKATPNSPRPLPGAPSPESK----- 576
DB 738 RRAPLSEGGHSLGCGYNNPMDGGSYTTLRPFEMNIPRTGDAESSEMQRPRPTCDDTVTYS 797

QY 577 ---KNQKKQYQ--LPSFPEPKSSTQAPESQSEELHYATLNPFGVPRPEAMPKGTQA 631
DB 798 ALHKRQGVGYENVIPDPFE-----DEGIHYSILQFGVGERPQAQ-----ENV 840

QY 632 DYAEVK 637
DB 841 DYVILK 846

RESULT 11
S50065
sialoadhesin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S50065
R:Crocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Milc
EMBO J. 13, 4490-4503, 1994
A:Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells
A:Reference number: S50065; MUID:95009950; PMID:7925291
A:Accession: S50065
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1694 <CRO>
A:Cross-references: UNIPROT:Q62230; EMBL:Z36293; NID:G557253; PIDN:CAA85290.1; PID:G55725

Query Match 8.4%; Score 282.5; DB 2; Length 1694;
Best Local Similarity 22.0%; Pred. No. 2.2e-10;
Matches 135; Conservative 71; Mismatches 199; Indels 209; Gaps 21;

QY 5 LLLSLGSGQMDGRFWIRVQSVVMVPEGLCTSVPCSPSYPRQDWTGTSTPAYGWFKA 64
DB 8 LLLASVSLQTTWG---VSSPNVQGLSGCLLICIFSYR-ADVPVSNGITAIWY--Y 61

QY 65 TETTKGAPVATNHSREVMSTRGRFQLTGDPAKNCSLVIRDAQWQDSQYFFRVERGS 124
DB 62 DYSGKRQWIHSGDKPLVDKRFGRGAEMLGMNDHDKVKNLLKDLKPEDSGTYNFRPEISD 121

QY 125 YVRNFNDGFFLKVTVLSTPRP----- 148
DB 122 SNRW-----LDVKGITTVTTDPSPTTIPPELREGMERNFNCSTPYCLQEKQVSLQ 175

QY 149 -----QDHTDLTCHVDFSRKGVSAQRTVRL 174
DB 176 WRGQDPTHSVTSFQSLPTGYSYHQTTLHWALSWQDHGRTLLC--QPSLGHSSRKEVYL 233

QY 175 RVAYAPRDLVISRTNDTPALEPQ-----QGVNPLYEAQK-----GQFLR- 215
DB 234 QVHAPKGVGEILLSSGNILPGDPVTLTCRVNSSYPVAVSQAQVARDGVNLGVTGHVRL 293


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Db 3398 SPTPTQV-----TPQLETKSIGASVEFHCAPVSDQGTQLRFKEGGLPPGSHVQDGVLR 3452
QY 354 LRVQVEHEGFTCHARHPLGSCVLSLSVHYSPKLL-----GPSCSWERAG 401
Db 3453 IQNLDQSCQGTVCQAHGFWKQAQASQLVIQALPSVLINTRTSVQTVVGHAVEFE--- 3509
QY 402 LHCSCSSQASPAFSLRWLWGEELLEGNSQDSFEVTPSSAGFWANSSLSLHGG----- 454
Db 3510 ----CLALGDPKQVTW-----SKVGHLPFGIVQSGGVVRIAHV 3545
QY 455 -LSSGLRRCRANVHGAQSGSILQPKKGLISTAFNGAFLGIGITALLFLCLA 509
Db 3546 ELADAGVRCATNAAGTQSHVLLVQALPQISMPOEVRVPAG---SAAVFPCTA 3598

RESULT 13
138000
Lutheran blood group glycoprotein precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C:Accession: I38000; S51663
R:Parsons, S.F.; Mallinson, G.; Holmes, C.H.; Houlihan, J.M.; Simpson, K.L.; Mawby, W.J.
Proc. Natl. Acad. Sci. U.S.A. 92, 5496-5500, 1995
A:Title: The Lutheran blood group glycoprotein, another member of the immunoglobulin sup
A:Reference number: I38000; MUID:95296337; PMID:7777537
A:Accession: I38000
A:Molecule type: mRNA
A:Residues: 1-628 <RES>
A:Cross-references: UNIPROT:P50895; EMBL:X83425; NID:G603559; PIDN:CAA58449.1; PID:G6035
A:Note: parts of this sequence, including the amino end of the mature form, were confirm
C:Genetics:
A:Gene: GDB:1U
A:Cross-references: GDB:120155; OMIM:111200
A:Map position: 19c12-19q13
C:Keywords: glycoprotein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-628/Product: Lutheran blood group glycoprotein #status experimental <MAT>

Query Match 7.4%; Score 251.5; DB 2; Length 628;
Best Local Similarity 23.3%; Pred. No. 6.7e-09;
Matches 162; Conservative 79; Mismatches 231; Indels 223; Gaps 40;

QY 5 LILSSLLGSSQAMDGFWIRVOESVWVPEGLCISVPCSFSPRODWTGSTPAYGY-WFKA 63
Db 17 LLLAVLLAAHPDAQAEVRLSVPLVEMVRGKSVILDCT---P---TGDHMYLWEP-- 67
QY 64 VTETTKGAP--VATNHQSREVMS---TRGR---FQLTGDPKGNCSLVIRDAQMDDESQ 115
Db 68 LIDRSGARPLASAEWQSGELQVTHDTRGSPFPQL---DSQGR--LVLAQAQVDEED 122
QY 116 YFFRVERG-----SYVRVNF----- 130
Db 123 YVCVVRAGAAGTAETARLNVFAKPEATEVSPNKGTLVWSDSAEATCNRSRNGNPAPK 182
QY 131 -----MN-DGFIKVTV-----LSFTP-----RPQDHTDLTCHVDPS 162
Db 183 ITWYRNGQLEVPVEMNPGYTSRTVRASGLLSLTSTLYLRKRDSDASFHCAHYIS 242
QY 163 ----RKXGSAQRTVRLRAYAPRDLVISRDNTPALEPQGNVPYLEAKQGFRLRLC 218
Db 243 LPEGRHRLDSPTFHLTLHPYEHVQFWVGSPTA-----GWV-----REGDTVQLLC 291
QY 219 ADDSQP-PATLSWLNQ---RVLSHSPWGPPLGLGLPCVKAGDSGRVTCBAENELQSQ 274
Db 292 RGDGSPSPYTLFRLQDEQEVNLNLEG-----NLTEGVTRGOSGTYGCRVEDYDAAD 346
QY 275 ----QALDLSVOY---PPENLRVWVSOANRTVLENLNGTSLFVLGOSLCLVCVTHSSP 328
Db 347 DVQLSTLRLVAYLDPLE-----LSEKVLSLPLNSSAVVNCVHGLP 390
QY 329 PARLSWTQRQVLSPSQSDPGVLELPRVQVHEGEFTCHA---RHPLGSHVLSLSVH 385
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Db 391 TPALRWTKOSTPL-----GDGPMLSSITFDNGTYVCEASLPTVPVLSRTQNFLLVQ 445
QY 386 YSPKL-----LGPSC--SW-EAEGLHCSCSSQASPAFSLRWLWGEELLEGNSQDSPEVTP 438
Db 446 GSELKTAETEPKADGSGWREGDEVTLICARGHPDKLSW-----SQLGSGPA---EPIP 497
QY 439 SSAGPWANSSLSLHGLSSGLR---LRCEAWNVHGAQS-----GSILQLPDKKG--LIST 488
Db 498 GRQG-WYSSSLTLK--VTSALSRDGISCEASNPHGNKRHVHFHGAVSPQTSQAGVAMAV 554
QY 489 AFGNAGFLGIGITALLFLCLALIMKILPKRRQTETPRPRFSRHSHTILDYINVVTAGP 548
Db 555 AVSVGLLL---LVVAVFYCV-----RR-----KGGP 577
QY 549 LAQRNOKATPNSPRTPLPFGAPS-PESKKNQKKQ 582
Db 578 CCRQRREKAP-----PGEFGLSHSGSQEPEQ 605

RESULT 14
A35648
B-cell adhesion protein CD22 alpha splice form precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 15-Mar-2004
C:Accession: A35648
R:Stamenkovic, I.; Seed, B.
Nature 345, 74-77, 1990
A:Title: The B-cell antigen CD22 mediates monocyte and erythrocyte adhesion.
A:Reference number: A35648; MUID:90231465; PMID:1691828
A:Accession: A35648
A:Molecule type: mRNA
A:Residues: 1-647 <STA>
A:Cross-references: GB:X52785; NID:G29778; PIDN:CAA36988.1; PID:G29779
C:Genetics:
A:Gene: GDB:CD22
A:Cross-references: GDB:127545; OMIM:107266
A:Map position: 19q13.1-19q13.1
C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; transmembr
F:1-19/Domain: signal sequence #status predicted <EXT>
F:20-510/Domain: extracellular #status predicted <EXT>
F:432-484/Domain: immunoglobulin homology <IMM>
F:511-529/Domain: transmembrane #status predicted <TM>
F:530-647/Domain: intracellular #status predicted <CYT>
F:67,101,112,135,164,231,268,302,397,457/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 7.3%; Score 245; DB 2; Length 647;
Best Local Similarity 21.9%; Pred. No. 1.9e-08;
Matches 133; Conservative 72; Mismatches 197; Indels 206; Gaps 26;

QY 1 MLLPLLLSSLLGSSQAMDGFWI-RVOESVWVPEGLCISVPCSFSP-----YPRQ 48
Db 3 LLGFWLLLLVLELAFSDSSKNVFEHPETLYANEGACVWIPCTYRALDGLSFILFHP 62
QY 49 DWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVMSRGRFQLTGDPKGNCSLVIRDA 108
Db 63 EYNKNTSKFD--GTRLYESTKDGKVP-----SEKRVQFGLGDKNK-NCTLSHPV 109
QY 109 QMDESQYFRVER----- 123
Db 110 HLNDSGQLGRMESKTEKMERIHLNVSRPPPHIQLPEIQESQEVTLTCLLNFSCYG 169
QY 124 SYVRFMNDGFFLK-----VTV-----LSFTPRPDHNTDLTCHVDFSRKGVIS 167
Db 170 YPIQLQMLLEGVPMRQAATVSTLSIKSVTRSELKSPQWSSHGKIVTCQLQADGKFL 229
QY 168 AQRVRLRAYAPRDLVISI-----SRDNTPALEPQPGQ--NVPI 205
Db 230 SNDTVQNVKHPKKVTVI-QNPMPIREGDVTILSCNYSNPSVTRYEMKPHGAWPEPS 289
QY 206 LEAQKGQFL-----RLCAADSQPPATLSWLNQ-----RV----- 236
Db 290 LVVLKIQNVGWDNTIACACNSWNASPVALNVQAPRDRVRKIKELPSLHSGNSVS 349
```

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QY 237 -----LSSHP-----W--GPRPLG-----LELPVKGAGDSRYTCRAENRLG-SQORALD 279
DB 350 LQDFSSHPKEVQFFWEXNGRLLGKESQINFDSISPDAGSYSCWVWNSIGQTASKAWT 409
QY 280 LSVQYPPENLRVMVSOANRTVLNGLNGTSLPVLQGSCLVCVTHSSPPAR-----LSWT 335
DB 410 LEVLYAPRRLRVKSMSPCDQ-----VMEKKSATLICESDANFPVSHYTFWFDN 456
QY 336 QROQVLSPOQSPDPGVLEPRVQVEHEGFTCHARHPLGSHQVLSL-LSVHYSPKLLGPS 394
DB 457 NQ-----SLPYHSQKRLLEPVKQVHSGAYWCQGTNSVCKGRSPLSLTLYVYSPETIGR 510
QY 395 CSWEAEGLH-----CSCSSQASAPSLRW-WLGEELLEGSSQDSFEV-----436
DB 511 V-----AVLGSCLAILIACGLKLR-----RWKRTSQOQLQENSSQGSFFVRNKKVR 561
QY 437 -TPSSAGP 443
DB 562 RAPLSEGP 569

RESULT 15
137202
B-CAM protein - human
C:Species: Homo sapiens (man)
G:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
W:Accession: I37202; S47272
R:Campbell, I.G.; Foulkes, W.D.; Senger, G.; Trowsdale, J.; Garin-Chesa, P.; Rettig, W.J.
Cancer Res. 54, 5761-5765, 1994
A:Title: Molecular cloning of the B-CAM cell surface glycoprotein of epithelial cancers:
A:Reference number: I37202; PMID:95042237; PMID:7954395
A:Accession: I37202
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-588 <RES>
A:Cross-references: UNIPROT:P50895; EMBL:X80036; NID:G535178; PIDN:CAA56327.1; PID:G5351
C:Genetics:
A:Gene: B-CAM

Query Match 7.1%; Score 239.5; DB 2; Length 588;
Best Local Similarity 23.1%; Pred. No. 3.8e-08;
Matches 155; Conservative 78; Mismatches 223; Indels 215; Gaps 38;

QY 5 LLLSSLLGGSQAMGDRFWIRVQESVMVPEGLCISVPCSFSPYRQDWTGTSTPAYGY-WFKA 63
DB 17 LLLAVLLAAHPDAQAEVRLSVPLVEMEGKSVILDT---P---TGTHDHYMLEWF-- 67
QY 64 VTETTKGAP--VATNHQSREVMSS---TRGR---PQLTGDPAKGNCSLVIRDAQMQDESQ 115
DB 68 LTDRSGARPLASAEHQSGSELOQVTHDTRGRSPYQL---DSQGR--LVLAEAQVGDGRD 122
QY 116 YPFRVERG-----SYRVYNF-----130
DB 123 YVCVVRAGAGTAATARLNVFAKPEATEVSFNKGTLSVMEDSAQEIATCNRSNGNPAPK 182
QY 131 -----NN-DGFFLKVTY-----LSFTP-----RPQHNITDLTCHVDPS 162
DB 183 ITWYRNGQRLVPEVMNPEGYMSTRVREASGLLSLTSTLYLPCRKDRDASFHCAAHYS 242
QY 163 ----RKGVSQAQTVRLVAVAPRDLVISISRONTALEPQPOGNVNPYLEAKQGFRLIC 218
DB 243 LPEGRHRLDSTFHLTHYPTEHVQVWGSPTFA-----GWV-----REGDTVQLIC 291
QY 219 AADSQP-PATLSWVLQN-----RVLSSSHMPGPRPLGLELPGVKAGDSGRYTCRAENRLGSQ 274
DB 292 RGDGSPSPHYTLFRLQDEQEVLNVNLEG-----NLTLGVTRGQSGTYGCKVEDYDAAD 346
QY 275 ----QKALDSVQY--PPENLRVMVSOANRTVLNGLNGTSLPVLQGSCLVCVTHSSP 328
DB 347 DVQLSKTLDRVAYLDPLE-----LSEGKVLSTFLNNSAVVNCVHGLP 390
QY 329 PARLSWTQRGOVLSQSPSDPGVLEPRVQVEHEGFTCHA---RHPLGSHQVLSLSVH 385
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DB 391 TPALRWTKDSTPL-----GDGPMLSLSSITFDNGTIVVCEASLFTVPVLSTQNTQFILLVQ 445
QY 386 YSPKL-----LQPSCL--SW-EAEGHLHCSQSQASAPSLRWMLGEELEGSSQDSFEVTP 438
DB 446 GSPELKTAETPEKADGWSREGDEVTLICSAARGHPDPKLSW---SQLGGSPA-----EPIP 497
QY 439 SSAGPWANSSLSLHGGILSSGLR---LRCEANNVHGAQS-----GSLQLQDPKKG--LIST 488
DB 498 GRQG-WYSSSLTLK--VTSALSRDGISCEASNPHGNKRVHVFHGAVSPQTSQAGVAVNAV 554
QY 489 AFSNCAFLGIGITALLFLCLALIIIMKILPKRRTQTETPRPRFSRHSHTILDYINWVPTAGP 548
DB 555 AVSVGLLL---LVAVFYCV-----RR-----KGGP 577
QY 549 LAQFRNOKATP 559
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Search completed: November 5, 2004, 13:51:06
Job time : 22.76s4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:53:32 ; Search time 109.924 Seconds
(without alignments)
2053.348 Million cell updates/sec

Title: US-09-937-636-4

Perfect score: 3377

Sequence: 1 MLLPILLSLLGGSQAMDGR.....RPEARMPKGTQDYAEVKFQ 639

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/FCT_NEW_PUB.pep.*
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4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/FCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
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18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
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20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3377	100.0	639	14	US-10-158-238-28
2	3354	99.3	639	10	US-09-984-130-33
3	3354	99.3	639	10	US-09-836-353A-33
4	3338	98.8	697	10	US-09-910-600-28
5	3334	98.7	697	10	US-09-984-130-149
6	3334	98.7	697	15	US-10-403-938-7
7	3334	98.7	697	16	US-10-614-853-10
8	3299	97.7	622	10	US-09-910-600-9
9	2803.5	83.0	544	9	US-09-910-600-8
10	2790.5	82.6	544	9	US-09-978-295A-259
11	2790.5	82.6	544	9	US-09-978-697-259
12	2790.5	82.6	544	9	US-09-978-192A-259
13	2790.5	82.6	544	9	US-09-999-832A-259

14	2790.5	82.6	544	10	US-09-978-189-259	Sequence 259, App
15	2790.5	82.6	544	10	US-09-978-608A-259	Sequence 259, App
16	2790.5	82.6	544	10	US-09-978-585A-259	Sequence 259, App
17	2790.5	82.6	544	10	US-09-978-191A-259	Sequence 259, App
18	2790.5	82.6	544	10	US-09-978-403A-259	Sequence 259, App
19	2790.5	82.6	544	10	US-09-978-564A-259	Sequence 259, App
20	2790.5	82.6	544	10	US-09-999-833A-259	Sequence 259, App
21	2790.5	82.6	544	10	US-09-981-915A-259	Sequence 259, App
22	2790.5	82.6	544	10	US-09-978-824-259	Sequence 259, App
23	2790.5	82.6	544	10	US-09-918-585A-259	Sequence 259, App
24	2790.5	82.6	544	10	US-09-999-834A-259	Sequence 259, App
25	2790.5	82.6	544	10	US-09-978-423A-259	Sequence 259, App
26	2790.5	82.6	544	10	US-09-978-193A-259	Sequence 259, App
27	2790.5	82.6	544	10	US-09-999-830A-259	Sequence 259, App
28	2790.5	82.6	544	10	US-09-978-757A-259	Sequence 259, App
29	2790.5	82.6	544	10	US-09-978-187B-259	Sequence 259, App
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31	2790.5	82.6	544	10	US-09-978-375A-259	Sequence 259, App
32	2790.5	82.6	544	10	US-09-978-298A-259	Sequence 259, App
33	2790.5	82.6	544	10	US-09-978-188A-259	Sequence 259, App
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36	2790.5	82.6	544	10	US-09-999-829A-259	Sequence 259, App
37	2790.5	82.6	544	10	US-09-978-299A-259	Sequence 259, App
38	2790.5	82.6	544	10	US-09-978-544A-259	Sequence 259, App
39	2790.5	82.6	544	10	US-09-978-665A-259	Sequence 259, App
40	2790.5	82.6	544	10	US-09-978-802A-259	Sequence 259, App
41	2790.5	82.6	544	11	US-09-999-831A-259	Sequence 259, App
42	2790.5	82.6	544	13	US-10-052-586-118	Sequence 118, App
43	2790.5	82.6	544	14	US-10-174-590-118	Sequence 118, App
44	2790.5	82.6	544	14	US-10-176-758-118	Sequence 118, App
45	2790.5	82.6	544	14	US-10-175-737-118	Sequence 118, App

ALIGNMENTS

RESULT 1

US-10-158-238-28
; Sequence 28, Application US/10158238
; Publication No. US20030040604A1

; GENERAL INFORMATION:

; APPLICANT: Immurex Corporation

; APPLICANT: Dirk, Anderson M.

; APPLICANT: Maken, John S.

; TITLE OF INVENTION: SIGLEC-12 POLYPEPTIDES, POLYNUCLEOTIDES, AND METHODS OF USE THEREC

; FILE REFERENCE: 3290-A

; CURRENT APPLICATION NUMBER: US/10158,238

; CURRENT FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: US 60/294,199

; PRIOR FILING DATE: 2001-05-29

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 28

; LENGTH: 639

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-158-238-28

Query Match		100.0%;	Score 3377;	DB 14;	Length 639;
Best Local Similarity		100.0%;	Pred. No. 2e-221;		
Matches 639;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MLLPILLSLLGGSQAMDGRFWRVQSVVMVPEGLCI-SVPCSFSPYPRQDWTGSTPAYGYW	60		
Db	1	MLLPILLSLLGGSQAMDGRFWRVQSVVMVPEGLCI-SVPCSFSPYPRQDWTGSTPAYGYW	60		
Qy	61	FKAVTTTKGAPVATNHQSRREVSTGRFOLTGDPAKNCSLVIRDAQMODESQYFRV	120		
Db	61	FKAVTTTKGAPVATNHQSRREVSTGRFOLTGDPAKNCSLVIRDAQMODESQYFRV	120		
Qy	121	BRGSVWFNFNDGFFLKVTVLSTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP	180		
Db	121	BRGSVWFNFNDGFFLKVTVLSTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP	180		

121 ERGSYVRYNPMNDGFFLKVTVLSTFTPRPDHNTDLTCHVDFFSRKGVSAQRTVRLRVAYAP 180
181 RDLVISISRDNTPALBPQGNVPYLEAOKGQFLRLCAADSPATLISWVLRVAYAP 240
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241 HPWGPRLGLELPGVKAGDSGRYTCRAENRLGSOQALDLSVQYPPENLRVWVSQANRTV 300
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301 LENLNGTSLPVLGGQSLCLVCTHSSPPARLSWTORGQVLSFSPQSDPGVLELPRVQVE 360
301 LENLNGTSLPVLGGQSLCLVCTHSSPPARLSWTORGQVLSFSPQSDPGVLELPRVQVE 360
361 HEGEFTCHARHPLGSOHVLSLSVHSPKLLGPSCSWEAEGHLHSCSSQASPAAPSLRWL 420
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421 GEELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCEAMNVHGAQSGSLQLP 480
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601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639
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RESULT 2

US-09-984-130-33
; Sequence 33, Application US/09984130
; Publication No. US2003005231A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-33

Query Match 99.3%; Score 3354; DB 10; Length 639;
Best Local Similarity 99.5%; Pred. No. 7.5e-220;
Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MLLPLLSLLGSGQAMDCGRFWIRVOESVNVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Db 1 MLLPLLSLLGSGQAMDCGRFWIRVOESVNVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Qy 61 FKAVTTTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120

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121 ERGSYVRYNPMNDGFFLKVTVLSTFTPRPDHNTDLTCHVDFFSRKGVSAQRTVRLRVAYAP 180
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181 RDLVISISRDNTPALBPQGNVPYLEAOKGQFLRLCAADSPATLISWVLRVAYAP 240
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481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPFRSHSTILDYI 540
481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPFRSHSTILDYI 540
541 NVVPTAGPLAQRNOKATPNSPRTPPLPGAPSPESKKNQKQYQLPSPFPKSSSTQAPES 600
541 NVVPTAGPLAQRNOKATPNSPRTPPLPGAPSPESKKNQKQYQLPSPFPKSSSTQAPES 600
601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639
601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639

RESULT 3

US-09-836-353A-33
; Sequence 33, Application US/09836353A
; Publication No. US20030129685A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/09/836,353A
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-353A-33

Query Match 99.3%; Score 3354; DB 10; Length 639;
Best Local Similarity 99.5%; Pred. No. 7.5e-220;
Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MLLPLLSLLGSGQAMDCGRFWIRVOESVNVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Db 1 MLLPLLSLLGSGQAMDCGRFWIRVOESVNVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Qy 61 FKAVTTTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120

61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDSEQYFFRV 120
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121 ERGSYRVNFMNDGFFLKVTLSFTPRQDHNHDTLCHVDFSRKGVSAQRTVRLVAYAP 180
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481 DKKGLISTAFNGAFIGIGITALLFLCLALIIIMKILPKRRTOTETPRPRFRSHSTILDYI 540
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601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639

RESULT 4
US-09-910-600-28
; Sequence 28, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,139
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L3-995-2
US-09-910-600-28
Query Match 98.8%; Score 3338; DB 10; Length 697;
Best Local Similarity 91.7%; Pred. No. 1e-218;
Matches 639; Conservative 0; Mismatches 0; Indels 58; Gaps 1;
QY 1 MLPLLLSLLGGSQAMDRFWRVQESVWVPEGLCISVPCSFSPYPRQDWTGSTPAYGW 60
DB 1 MLPLLLSLLGGSQAMDRFWRVQESVWVPEGLCISVPCSFSPYPRQDWTGSTPAYGW 60
QY 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDSEQYFFRV 120

61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDSEQYFFRV 120
121 ERGSYRVNFMNDGFFLKVTLSFTPRQDHNHDTLCHVDFSRKGVSAQRTVRLVAYAP 140
121 ERGSYRVNFMNDGFFLKVTLSFTPRQDHNHDTLCHVDFSRKGVSAQRTVRLVAYAP 180
141 -----VLSFTPRQDHNHDTLCHVDFSRKGVSAQRTVRLVAYAP 182
181 TGAALSSQGTPTTSHFSVLSFTPRQDHNHDTLCHVDFSRKGVSAQRTVRLVAYAP 240
183 LVISIRSDNTPALEPOQGNVPYLEAKGQFLRLCAADSOPPATLSWLQNRVLSSSHP 242
241 LVISIRSDNTPALEPOQGNVPYLEAKGQFLRLCAADSOPPATLSWLQNRVLSSSHP 300
243 WGRPRPLGLELPGVKAGDSGRYTCAENRLGSOQRALDLSVQYPPENLRVMVSOANRTVLE 302
301 WGRPRPLGLELPGVKAGDSGRYTCAENRLGSOQRALDLSVQYPPENLRVMVSOANRTVLE 360
303 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQRGQVLSPPSPDPGVLELPRVQVEHE 362
361 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQRGQVLSPPSPDPGVLELPRVQVEHE 420
363 GEFTCHARHPLGSHQVLSLSVHYSPKLLGSPCSWEAEGHLCSSQASPAFLRWLGE 422
421 GEFTCHARHPLGSHQVLSLSVHYSPKLLGSPCSWEAEGHLCSSQASPAFLRWLGE 480
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481 ELLEGNSQDSFEVTPSSAGFWANSSLSLHGGSSGLRLRCEAWNVHGAQSGSILQLPDK 540
483 KGLISTAFNGAFIGIGITALLFLCLALIIIMKILPKRRTOTETPRPRFRSHSTILDYIN 542
541 KGLISTAFNGAFIGIGITALLFLCLALIIIMKILPKRRTOTETPRPRFRSHSTILDYIN 600
543 VPTAGPLAQRNOKATNSPRTPLPGCAPSPESKQKQYQLPSPFPKSSSTQAPESQE 602
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603 QSEELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639
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RESULT 5
US-09-984-130-149
; Sequence 149, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489F2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 149
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-149
Query Match 98.7%; Score 3334; DB 10; Length 697;
Best Local Similarity 91.5%; Pred. No. 1.9e-218;

Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY 1 MLLPILLSLLGSGQAMDRFWIRVQESVMVPEGLCISVPCFSYPRQDWTGTTPAYGYW 60
 DB 1 MLLPILLSLLGSGQAMDRFWIRVQESVMVPEGLCISVPCFSYPRQDWTGTTPAYGYW 60
 QY 61 FKAVTETTKGAPVATNHOSREVENSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
 DB 61 FKAVTETTKGAPVATNHOSREVENSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
 QY 121 ERGSYVRYNFMNDGFFLKVT----- 140
 DB 121 ERGSYVRYNFMNDGFFLKVTALTKQPDVYIPETLEPGQPVTVICVFNWAFEECPSPFSW 180
 QY 141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAPRD 182
 DB 181 TGAALSSQGTTPITSHFVSLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAPRD 240
 QY 183 LVISISRDNTPALEPQPGNVPLYEAQKQGLRLCAADSQPPATLSWLQNRVLSSSH 242
 DB 241 LVISISRDNTPALEPQPGNVPLYEAQKQGLRLCAADSQPPATLSWLQNRVLSSSH 300
 QY 243 WGRPRPLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVSAQNRVLE 302
 DB 301 WGRPRPLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVSAQNRVLE 360
 QY 303 NLGNGTSLPVLEQSLCLVCTHSSPPARLSWTORGQVLSPOSDPGVLELPRVQVEHE 362
 DB 361 NLGNGTSLPVLEQSLCLVCTHSSPPARLSWTORGQVLSPOSDPGVLELPRVQVEHE 420
 QY 363 GEFTCHARHPLGSHVLSLSVHSPKLLGPCSWAEAGLHCSCSQASAPSLRWMLGE 422
 DB 421 GEFTCHARHPLGSHVLSLSVHSPKLLGPCSWAEAGLHCSCSQASAPSLRWMLGE 480
 QY 423 ELLEGNSQDSFEVTPSSAGPWANSSLSHGGLSSGLRLRCEANVHGAQSGSILQLPDK 482
 DB 481 ELLEGNSQDSFEVTPSSAGPWANSSLSHGGLSSGLRLRCEANVHGAQSGSILQLPDK 540
 QY 483 KGLISTAFNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRFRSHSTILDYINV 542
 DB 541 KGLISTAFNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRFRSHSTILDYINV 600
 QY 543 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSTQAPESQE 602
 DB 601 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSTQAPESQE 660
 QY 603 SQBELHYATLNFPGVRPEARMKGTQADYAEVKFQ 639
 DB 661 SQBELHYATLNFPGVRPEARMKGTQADYAEVKFQ 697

RESULT 6

US-10-403-938-7
 Sequence 7, Application US/10403938
 Publication No. US20040025195A1
 GENERAL INFORMATION:
 APPLICANT: Bristol-Myers Squibb Company
 TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
 TYPE: PRT
 FILE REFERENCE: D0227 NP
 CURRENT APPLICATION NUMBER: US/10/403,938
 CURRENT FILING DATE: 2003-03-28
 PRIOR APPLICATION NUMBER: U.S. 60/368,422
 PRIOR FILING DATE: 2002-03-28
 NUMBER OF SEQ ID NOS: 86
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 7
 LENGTH: 697
 ORGANISM: Homo sapiens
 US-10-403-938-7

Query Match

98.7%; Score 3334; DB 15; Length 697;

Best Local Similarity 91.5%; Pred. No. 1.9e-218;
 Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY 1 MLLPILLSLLGSGQAMDRFWIRVQESVMVPEGLCISVPCFSYPRQDWTGTTPAYGYW 60
 DB 1 MLLPILLSLLGSGQAMDRFWIRVQESVMVPEGLCISVPCFSYPRQDWTGTTPAYGYW 60
 QY 61 FKAVTETTKGAPVATNHOSREVENSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
 DB 61 FKAVTETTKGAPVATNHOSREVENSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
 QY 121 ERGSYVRYNFMNDGFFLKVT----- 140
 DB 121 ERGSYVRYNFMNDGFFLKVTALTKQPDVYIPETLEPGQPVTVICVFNWAFEECPSPFSW 180
 QY 141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAPRD 182
 DB 181 TGAALSSQGTTPITSHFVSLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAPRD 240
 QY 183 LVISISRDNTPALEPQPGNVPLYEAQKQGLRLCAADSQPPATLSWLQNRVLSSSH 242
 DB 241 LVISISRDNTPALEPQPGNVPLYEAQKQGLRLCAADSQPPATLSWLQNRVLSSSH 300
 QY 243 WGRPRPLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVSAQNRVLE 302
 DB 301 WGRPRPLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVSAQNRVLE 360
 QY 303 NLGNGTSLPVLEQSLCLVCTHSSPPARLSWTORGQVLSPOSDPGVLELPRVQVEHE 362
 DB 361 NLGNGTSLPVLEQSLCLVCTHSSPPARLSWTORGQVLSPOSDPGVLELPRVQVEHE 420
 QY 363 GEFTCHARHPLGSHVLSLSVHSPKLLGPCSWAEAGLHCSCSQASAPSLRWMLGE 422
 DB 421 GEFTCHARHPLGSHVLSLSVHSPKLLGPCSWAEAGLHCSCSQASAPSLRWMLGE 480
 QY 423 ELLEGNSQDSFEVTPSSAGPWANSSLSHGGLSSGLRLRCEANVHGAQSGSILQLPDK 482
 DB 481 ELLEGNSQDSFEVTPSSAGPWANSSLSHGGLSSGLRLRCEANVHGAQSGSILQLPDK 540
 QY 483 KGLISTAFNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRFRSHSTILDYINV 542
 DB 541 KGLISTAFNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRFRSHSTILDYINV 600
 QY 543 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSTQAPESQE 602
 DB 601 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSTQAPESQE 660
 QY 603 SQBELHYATLNFPGVRPEARMKGTQADYAEVKFQ 639
 DB 661 SQBELHYATLNFPGVRPEARMKGTQADYAEVKFQ 697

RESULT 7

US-10-614-853-10
 Sequence 10, Application US/10614853
 Publication No. US20040138114A1
 GENERAL INFORMATION:
 APPLICANT: HENRY CHIU
 APPLICANT: HILARY CLARK
 APPLICANT: KATHRYN DENNIS
 APPLICANT: SHERMAN FONG
 APPLICANT: JILL SCHOENFELD
 APPLICANT: WILLIAM WOOD
 APPLICANT: THOMAS WU
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
 TITLE OF INVENTION: RELATED DISEASES
 FILE REFERENCE: PI9731-10
 CURRENT APPLICATION NUMBER: US/10/614,853
 CURRENT FILING DATE: 2003-07-08
 PRIOR APPLICATION NUMBER: US 60/394,485
 PRIOR FILING DATE: 2002-07-08
 NUMBER OF SEQ ID NOS: 28
 SEQ ID NO 10


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; LENGTH: 697
; SEQ ID NO 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-614-853-10

Query Match      98.7%; Score 3334; DB 16; Length 697;
Best Local Similarity 91.5%; Pred. No. 1.9e-218;
Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

Qy 1 MLLPILLSLGGSOAMDGRFIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
Db 1 MLLPILLSLGGSOAMDGRFIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
Qy 61 FXAVTETTKGAPVATNHOSREVMETGRFOLITGDPKAGNCSLVIRDAQMDQESQYFPRV 120
Db 61 FXAVTETTKGAPVATNHOSREVMETGRFOLITGDPKAGNCSLVIRDAQMDQESQYFPRV 120
Qy 121 ERGSYVRVYFMNDGFLKVT----- 140
Db 121 ERGSYVRVYFMNDGFLKVTALQKPDVVIPTLEPGQPVTVICVFNWAFECPPPSFW 180
Qy 141 -----VLSTPRPDQDHTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 182
Db 181 TGAALSSQGTKEPTSHFVLSLTPRQDHTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 240
Qy 183 LVISIRDNTPALEPOQGNVPILEAQKQFRLILCAADSOPTATLSWLQNRVLSSHP 242
Db 241 LVISIRDNTPALEPOQGNVPILEAQKQFRLILCAADSOPTATLSWLQNRVLSSHP 300
Qy 243 WGPRLPLGLELPGVAKGDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLE 302
Db 301 WGPRLPLGLELPGVAKGDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLE 360
Qy 303 NLNGTSLPLVEGQSCLVCVTHSSPPARLSWTORGQVLSPPQSDPGVLELPRVQVEHE 362
Db 361 NLNGTSLPLVEGQSCLVCVTHSSPPARLSWTORGQVLSPPQSDPGVLELPRVQVEHE 420
Qy 363 GFPTCHARPLGSOHVLSLSVHYSPKILGPCSWEAEGHCSQSPASPSLRWLGE 422
Db 421 GFPTCHARPLGSOHVLSLSVHYSPKILGPCSWEAEGHCSQSPASPSLRWLGE 480
Qy 423 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGGLSGRLRCEAMNVHGAQSGSILQLPDK 482
Db 481 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGGLSGRLRCEAMNVHGAQSGSILQLPDK 540
Qy 483 KGLISTAFSNGAPFLGIGITALLFLCLALIMKILPKRTOTETPRFRSRHSTILDYINV 542
Db 541 KGLISTAFSNGAPFLGIGITALLFLCLALIMKILPKRTOTETPRFRSRHSTILDYINV 600
Qy 543 VPTAGPLAOKRQKATPNSPRTPLPAGAPSPESKKNQKQYQLPSFPPEKSTQAPESQE 602
Db 601 VPTAGPLAOKRQKATPNSPRTPLPAGAPSPESKKNQKQYQLPSFPPEKSTQAPESQE 660
Qy 603 SOBELHYATLNFPGVPRPEARMKPGTQADYAEVKFQ 639
Db 661 SOBELHYATLNFPGVPRPEARMKPGTQADYAEVKFQ 697
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RESULT 8
US-09-910-600-9
; Sequence 9, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,139
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-600-9

Query Match      97.7%; Score 3299; DB 10; Length 622;
Best Local Similarity 100.0%; Pred. No. 4e-216;
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 DGRFWIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYWFKAVTETTKGAPVATNH 77
Db 1 DGRFWIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYWFKAVTETTKGAPVATNH 60
Qy 78 QSREVMETGRFOLITGDPKAGNCSLVIRDAQMDQESQYFPRVERGSYVRVYFMNDGFFL 137
Db 61 QSREVMETGRFOLITGDPKAGNCSLVIRDAQMDQESQYFPRVERGSYVRVYFMNDGFFL 120
Qy 138 KTVILSTPRPDQDHTDLTCHVDFSRKGVSAQRTVRLRAYAPRDVILSRNTPALEP 197
Db 121 KTVILSTPRPDQDHTDLTCHVDFSRKGVSAQRTVRLRAYAPRDVILSRNTPALEP 180
Qy 198 QPQGNVPILEAQKQFRLILCAADSOPTATLSWLQNRVLSSHPGPRPLGLELPGVKA 257
Db 181 QPQGNVPILEAQKQFRLILCAADSOPTATLSWLQNRVLSSHPGPRPLGLELPGVKA 240
Qy 258 GDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLELNGTSLPLVEGQS 317
Db 241 GDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLELNGTSLPLVEGQS 300
Qy 318 LCLVCVTHSSPPARLSWTORGQVLSPPQSDPGVLELPRVQVEHEGFTCHARHPLGSOH 377
Db 301 LCLVCVTHSSPPARLSWTORGQVLSPPQSDPGVLELPRVQVEHEGFTCHARHPLGSOH 360
Qy 378 VLSLSVHYSPKILGPCSWEAEGHCSQSPASPSLRWLGEELLEGNSQDSFEVT 437
Db 361 VLSLSVHYSPKILGPCSWEAEGHCSQSPASPSLRWLGEELLEGNSQDSFEVT 420
Qy 438 PSSAGPWANSSLSLHGGLSGRLRCEAMNVHGAQSGSILQLPDKKGLISTAFSNGAPFLG 497
Db 421 PSSAGPWANSSLSLHGGLSGRLRCEAMNVHGAQSGSILQLPDKKGLISTAFSNGAPFLG 480
Qy 498 IGITALLFLCLALIMKILPKRTOTETPRFRSRHSTILDYINVVPTAGPLAOKRQK 557
Db 481 IGITALLFLCLALIMKILPKRTOTETPRFRSRHSTILDYINVVPTAGPLAOKRQK 540
Qy 558 TPNSPRTPLPAGAPSPESKKNQKQYQLPSFPPEKSTQAPESQESBELHYATLNFPGV 617
Db 541 TPNSPRTPLPAGAPSPESKKNQKQYQLPSFPPEKSTQAPESQESBELHYATLNFPGV 600
Qy 618 RPRPEARMKPGTQADYAEVKFQ 639
Db 601 RPRPEARMKPGTQADYAEVKFQ 622
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RESULT 9
US-09-910-600-8
; Sequence 8, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,139
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
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LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
US-09-910-600-8

Query Match      83.0%; Score 2803.5; DB 10; Length 544;
Best Local Similarity 85.1%; Pred. No. 1.9e-182;
Matches 544; Conservative 0; Mismatches 0; Indels 95; Gaps 1;

QY 1 MLLPLLSSLLGGSOAGDRFWIRVQESVVMPEGLCISVPCSFSPRQDWTGSTPAYGYW 60
Db 1 MLLPLLSSLLGGSOAGDRFWIRVQESVVMPEGLCISVPCSFSPRQDWTGSTPAYGYW 60
QY 61 PKAVTETTKGAPVATNHQSREVENSTGRFQLTCDPAKNCSLVIRDAQMODESQYFRV 120
Db 61 PKAVTETTKGAPVATNHQSREVENSTGRFQLTCDPAKNCSLVIRDAQMODESQYFRV 120
QY 121 ERGSYVRVYFMNDGFFLKVTVLSFTPRPDHNTDLTCHVDFSRKGVSAQRVRLVAYAP 180
Db 121 ERGSYVRVYFMNDGFFLKVTVLSFTPRPDHNTDLTCHVDFSRKGVSAQRVRLVAYAP 180
QY 181 RDLVISISRDNTPALEPQPGNVPLYEAQKGQFLRLCCAOSQPPATLSWLQNRVLSSS 240
Db 181 RDLVISISRDNTPALEPQPGNVPLYEAQKGQFLRLCCAOSQPPATLSWLQNRVLSSS 240
QY 241 HPWGPRPLGLLELPGVKAGDSGRVTCRAENRLGSOQRALDLSVOYDPENLRVWVSCARV 300
Db 241 HPWGPRPLGLLELPGVKAGDSGRVTCRAENRLGSOQRALDLSVOYDPENLRVWVSCARV 300
QY 301 LENLNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGOVLSPSQSPDPGVLELPRVQVE 360
Db 301 LENLNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGOVLSPSQSPDPGVLELPRVQVE 360
QY 361 HEGEFTCHARHPLGSOHVLSLSVHVSYPKLLGPSCSWAEGLHCSCSSQASPAFLRWL 420
Db 361 HEGEFTCHARHPLGSOHVLSLSVHVSYPKLLGPSCSWAEGLHCSCSSQASPAFLRWL 420
QY 421 GEELLEGNSQDSPEVTFSSAGPWANSLSLHGLSSGLRLRCEAWNHHGAQSILQLP 480
Db 387 ----- 386
QY 481 DKKGLISTAFNGAFIGITALLPFLCLALIMKILPKRTQTETPRPRSRHSHTILDYI 540
Db 387 -KKGLISTAFNGAFIGITALLPFLCLALIMKILPKRTQTETPRPRSRHSHTILDYI 445
QY 541 NVVTFAGPLAQKNQKATPNSRPTLPFGCAPSPESKQKQYQLPFPEPKSTQAPES 600
Db 446 NVVTFAGPLAQKNQKATPNSRPTLPFGCAPSPESKQKQYQLPFPEPKSTQAPES 505
QY 601 QESQEEHLHYATLNFPGVRRPPEARMKPGTDIAYEVKEQ 639
Db 506 QESQEEHLHYATLNFPGVRRPPEARMKPGTDIAYEVKEQ 544

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```

1  APPLICANT: Gurney, Austin L.
2  APPLICANT: Hillar, Kenneth J
3  APPLICANT: Kijavin, Ivar J.
4  APPLICANT: Kuc, Sophia S.
5  APPLICANT: Napier, Mary A.
6  APPLICANT: Pan, James,
7  APPLICANT: Paoni, Nicholas F.
8  APPLICANT: Roy, Margaret Ann
9  APPLICANT: Shelton, David L.
10 APPLICANT: Stewart, Timothy A.
11 APPLICANT: Tumas, Daniel
12 APPLICANT: Williams, P. Mickey
13 APPLICANT: Wood, William I
14
15 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
16
17 TITLE OF INVENTION: Acids Encoding the Same
18
19 FILE REFERENCE: P2630P1C11
20
21 CURRENT APPLICATION NUMBER: US/09/978,295A
22
23 CURRENT FILING DATE: 2001-10-15
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25 PRIOR APPLICATION NUMBER: 09/918585
26
27 PRIOR FILING DATE: 2001-07-30
28
29 PRIOR APPLICATION NUMBER: 60/062250
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31 PRIOR FILING DATE: 1997-10-17
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 ; PRIOR APPLICATION NUMBER: 60/080327
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; PRIOR APPLICATION NUMBER: 60/084441
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 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
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 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.6%; Score 2790.5; DB 9; Length 544;
 Best Local Similarity 84.8%; Pred. No. 1.5e-181;
 Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;

Qy	1	MLPPLLSLLGGSQAMDFWIRVQESVMVPEGLCLISVPCSFSPQDWTGTPAYGYW	60
Db	1	MLPPLLSLLGGSQAMDFWIRVQESVMVPEGLCLISVPCSFSPQDWTGTPAYGYW	60
Qy	61	FKAVTETTKGAPVATNHQREVENMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFVR	120
Db	61	FKAVTETTKGAPVATNHQREVENMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFVR	120
Qy	121	ERGSYVRYNFMNDGFFLKVTVLSTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP	180
Db	121	ERGSYVTYNFMNDGFFLKVTVLSTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP	180
Qy	181	RDLVISIRSDNTPALEPQPGQNVPLYEAKQGFRLICAADSOPTATLSWVLQNRVLSSS	240
Db	181	RDLVISIRSDNTPALEPQPGQNVPLYEAKQGFRLICAADSOPTATLSWVLQNRVLSSS	240
Qy	241	HPWGPRLGLGLPGVKAGDSGRYTCRAENRIGSQORALDLSVQYPPENLRVMVSOANRTV	300
Db	241	HPWGPRLGLGLPGVKAGDSGRYTCRAENRIGSQORALDLSVQYPPENLRVMVSOANRTV	300
Qy	301	LENLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQGVLSPSQSPDGPVLELPRVQVE	360
Db	301	LENLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQGVLSPSQSPDGPVLELPRVQVE	360
Qy	361	HEGEFTCHARHPLGSOHVLSLSVHVSFKLLGPSCSWEAEGHSCSSQASPAFSLRWL	420
Db	361	HEGEFTCHARHPLGSOHVLSLSVHVSFKLLGPSCSWEAEGHSCSSQASPAFSLRWL	420
Qy	421	GEELLEGNSQDSPEVTPSSAGPWANSSLSLHGGLSLRURCEANVHGAQSGSILQLP	480
Db	387	-----	386

; PRIOR FILING DATE: 1998-04-22
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.8%; Score 2790.5; DB 9; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.5e-181;

Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;
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Db |||||
Qy 1 MLLPLLLSSLLGGSQAMDGFRWIRVOESVMVPEGLCISVPCSFSPRQDWTGTPAYGYW 60
Db |||||
Qy 61 FKAVTTTKGAPVATNHQREVENMSTRGRPOLFGDPAKGNCSLVIRDAQMDSSQYFFRV 120
Db |||||
Qy 61 FKAVTTTKGAPVATNHQREVENMSTRGRPOLFGDPAKGNCSLVIRDAQMDSSQYFFRV 120
Db |||||
Qy 121 ERGSYRYNEMNDGFFLKVTLSFTPRPDHNDLJCHVDVFSRKGVSQARTVRLVAYAP 180
Db |||||
Qy 121 ERGSYRYNEMNDGFFLKVTLSFTPRPDHNDLJCHVDVFSRKGVSQARTVRLVAYAP 180
Db |||||
Qy 181 RDLVISISRDNTPALEPQPGQNPVYLEAQKGQFLRLCAADSOPPATLSWVLQNRVLSSS 240
Db |||||
Qy 241 HPWGPRPLGLELPQVAGDSGRYTCRAENPLGSOQALDLSVOYPENLRVMYSQANRTV 300
Db |||||
Qy 241 HPWGPRPLGLELPQVAGDSGRYTCRAENPLGSOQALDLSVOYPENLRVMYSQANRTV 300
Db |||||
Qy 301 LENLNGTSLPVLGGOSLCLVVCVTHSSPPARLSWTORGQVLSPSQSPDPCVLELPRVQVE 360
Db |||||
Qy 301 LENLNGTSLPVLGGOSLCLVVCVTHSSPPARLSWTORGQVLSPSQSPDPCVLELPRVQVE 360
Db |||||
Qy 361 HEGEFTCHARHPLGSHVLSLSVHSPKLLGSPCSWEAEGLHCSQSPASPAWSLWLL 420
Db |||||
Qy 361 HEGEFTCHARHPLGSHVLSLSVHSPKLLGSPCSWEAEGLHCSQSPASPAWSLWLL 420
Db |||||
Qy 421 GBEELGESSQDSFEVTPSSAGPWANSSLSLHGGSLRCEAMNVHGAQSGSILQLP 480
Db |||||
Qy 481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQETPRPRFSRHSHTILDYI 540
Db |||||
Qy 541 NVVPTAGPLAQKQKATPNSPRTPLPPGAPSPESKKNOKKQYQLSPFPKSKSTQAPES 600
Db |||||
Qy 601 QESQELHYATLNFPPGVPRPPEARMMPKGTQADYAEVKFQ 639
Db |||||
Qy 606 QESQELHYATLNFPPGVPRPPEARMMPKGTQADYAEVKFQ 544
Db |||||
RESULT 12
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; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Forst, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.6%; Score 2790.5; DB 9; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.5e-181; Indels 95; Gaps 1;
Matches 542; Conservative 0; Mismatches 2;

Qy 1 MLLPILLSLLGSGQAMGRFWIRVOESVMYPEGICISVPCSFYPRODWTGSTPAYGYW 60
Db 1 MLLPILLSLLGSGQAMGRFWIRVOESVMYPEGICISVPCSFYPRODWTGSTPAYGYW 60
Qy 61 FKAVTETTKGAPVATNHQSRREVEMSTRGRFQITGDPKAGNCSLVIRDAQMDESOYFRV 120
Db 61 FKAVTETTKGAPVATNHQSRREVEMSTRGRFQITGDPKAGNCSLVIRDAQMDESOYFRV 120
Qy 121 ERGSVVRNFMNDGFELKTVLSFTFRPDQNDTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
Db 121 ERGSVVRNFMNDGFELKTVLSFTFRPDQNDTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
Qy 181 RDLVISISRDNTPALEPOQGNVPYLEAKGQFRLLLCAADSPQPPATLSWYLNQNVLS 240
Db 181 RDLVISISRDNTPALEPOQGNVPYLEAKGQFRLLLCAADSPQPPATLSWYLNQNVLS 240
Qy 241 HPWGRPRIGLELPGYKAGDSGRYTCAENRLGSOQRALDLSVOYPPENLRVMVQANRTV 300
Db 241 HPWGRPRIGLELPGYKAGDSGRYTCAENRLGSOQRALDLSVOYPPENLRVMVQANRTV 300
Qy 301 LENLNGTSLPVLGQSLCLVCTVTHSSPPARLSWTQGVLSPOSPDPGVLELPRVOVE 360
Db 301 LENLNGTSLPVLGQSLCLVCTVTHSSPPARLSWTQGVLSPOSPDPGVLELPRVOVE 360
Qy 361 HEGEFTCHARPLGSGHVSLSVHYSPKLLGPSCSWEABGLHCSCSSQASPAFLRWL 420
Db 361 HEGEFTCHARPLGSGHVSLSVHY----- 386
Qy 421 GEELEGNSSQDSFEVTPSSAGFPWANSSLSLHGLSSGLRURCEAWNVHGAQSGSILQLP 480
Db 387 ----- 386
Qy 481 DKKGLISTAFNSGAFIGITALLFLCLALIMKILPKRTQTETPRFRSRHSTILDYI 540
Db 387 -KKGLISTAFNSGAFIGITALLFLCLALIMKILPKRTQTETPRFRSRHSTILDYI 445
Qy 541 NVVPTAGPLAQKNOKATPNSRTPLPQAGSPESKKNQKQYQLPSPEPKSSTQAPES 600
Db -----

Db 446 NVVPTAGPLAQKNOKATPNSRTPPPPGAPSPESKKNQKQYQLPSPEPKSSTQAPES 505
Qy 601 QESQELHYATLNFPGVRRPRPEARMKPGTQADYAEVKFQ 639
Db 506 QESQELHYATLNFPGVRRPRPEARMKPGTQADYAEVKFQ 544

RESULT 13
US-09-999-832A-259
Sequence 259, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.6%; Score 2790.5; DB 9; Length 544;

Best Local Similarity 84.8%; Pred. No. 1.5e-181;

Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;

Qy 1 MLLPILLSLLGGSQAMGRFIRVQESVWVPEGLICISVPCFSYPRQDWTGSTPAYGYW 60

Db 1 MLLPILLSLLGGSQAMGRFIRVQESVWVPEGLICISVPCFSYPRQDWTGSTPAYGYW 60

Qy 61 FXAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKGNCSLVIRDAQMDSQYFFRV 120

Db 61 FFAVTEETKGAFAVATNHOSEVEMSTRGRFOLTGDPKAGNCSLVIRDAQMDSEQYFFRV 120
QY 121 BRGSVRYNFMNDGFELKVTYVTFPRQDNDTDLTCHVDPSRKGVSAQRTVRLRVAYAP 180
Db 121 BRGSVRYNFMNDGFELKVTYVTFPRQDNDTDLTCHVDPSRKGVSAQRTVRLRVAYAP 180
QY 181 RDLVISIRDNTPALEPQPGNVVYLEAQKGFLLCAADSQPPATLSWVLRNVLSSS 240
Db 181 RDLVISIRDNTPALEPQPGNVVYLEAQKGFLLCAADSQPPATLSWVLRNVLSSS 240
QY 241 HPGWRPLGLEPGVKAGDSGRYTCAENRGLSQQRALDLSVOYPPENLRVWVSOANRTV 300
Db 241 HPGWRPLGLEPGVKAGDSGRYTCAENRGLSQQRALDLSVOYPPENLRVWVSOANRTV 300
QY 301 LENLNGTSLPVLQSGSLCLVCTVTHSSPPARLSWTQRQVLSPSPQSPDGVLELPRVQVE 360
Db 301 LENLNGTSLPVLQSGSLCLVCTVTHSSPPARLSWTQRQVLSPSPQSPDGVLELPRVQVE 360
QY 361 HEGEFTCHARHPLGSHQVLSLSVHYSKLLGPSCSWAEGHLHCSCSSQASPAFSLRWL 420
Db 361 HEGEFTCHARHPLGSHQVLSLSVHYSKLLGPSCSWAEGHLHCSCSSQASPAFSLRWL 420
QY 421 GSELLEGSSQDSFEVTPSSAGPWANSLSLHGLSSGLRLRCEAWNVHGAQSGSILQLP 480
Db 387 ----- 386
QY 481 DKKGLISTAFNSGAFIGITALLFLCLALIMKILPKRRTQETPRFRSRHSTILDYI 540
Db 387 -KKGLISTAFNSGAFIGITALLFLCLALIMKILPKRRTQETPRFRSRHSTILDYI 445
QY 541 NVVPTAGPLAQRNOKATPNSPRTPLPGAPSPESKQKQYQYQYQYQYQYQYQYQY 600
Db 446 NVVPTAGPLAQRNOKATPNSPRTPLPGAPSPESKQKQYQYQYQYQYQYQYQYQY 505
QY 601 QBSQBELHYATLNFVGVRPRPEARMKPGTQADYAEVKFQ 639
Db 506 QBSQBELHYATLNFVGVRPRPEARMKPGTQADYAEVKFQ 544

RESULT 14

US-09-978-189-259

Sequence 259, Application US/09978189

Publication No. US20030004102A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.6%; Score 2790.5; DB 10; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.5e-181;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;

QY 1 MLLPLLSSLLGGSQAMDGRFWRVQESVMVPEGLCISVPCSFSPQDWTGTPAYGYW 60
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QY 61 PKAVTETTKGAPVATNHSREVENSTGRFQLTGDDPAKNCSLVIRDAQMDSSQYFFRV 120
DB 61 PKAVTETTKGAPVATNHSREVENSTGRFQLTGDDPAKNCSLVIRDAQMDSSQYFFRV 120

QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDQDHTDLTCHVDFSRKGSQAQTVRLRVAYAP 180
DB 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDQDHTDLTCHVDFSRKGSQAQTVRLRVAYAP 180

QY 181 RDLVISRONTFALESPOQGNVPYLEAQKQFLRLCAADSPATLSWLVQNRVLS 240
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DB 241 HPWGPRLGLELPGVKAGDSGRYTCRAENRLGSOQRAALDLSVQYPPENLRVMVSQANRTV 300

QY 301 LENLGNQTSPLVLEGQSLCVVTHSSPPARLSWTORGQVLSQSDPDGVLELPRVQVE 360
DB 301 LENLGNQTSPLVLEGQSLCVVTHSSPPARLSWTORGQVLSQSDPDGVLELPRVQVE 360

QY 361 HEGFTCHARHPLGSHVLSLSVHYSPLGLGSCSNEABGLHCSCSSQASPAESLRWWL 420
DB 361 HEGFTCHARHPLGSHVLSLSVHYSPLGLGSCSNEABGLHCSCSSQASPAESLRWWL 420

QY 421 GEELLEGNSQDSFEVTFSSAGPWANSSLSLHGGLSSGLRCEANVHGAQSGSILQLP 480
DB 387 ----- 386

QY 481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTOTETPRPRSRHSTILDYI 540
DB 387 -KKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTOTETPRPRSRHSTILDYI 445

QY 541 NVVPTAGLAQKXNQKATPNSRTPPPGAPSPESKKNQKQYQLPSFPPEPKSSTQAPES 600
DB 446 NVVPTAGLAQKXNQKATPNSRTPPPGAPSPESKKNQKQYQLPSFPPEPKSSTQAPES 505

QY 601 QESQELHYATLNFPGVRRPEARMFKGTQADYAEVKFQ 639
DB 506 QESQELHYATLNFPGVRRPEARMFKGTQADYAEVKFQ 544

RESULT 15

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; Sequence 259, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 259
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-259
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Query Match      82.6%; Score 2790.5; DB 10; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.5e-181;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;
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Db      1  MLPLLLSLLGSGQAWDGRFWRVCEVYVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Qy     61  FRAVTEITTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
Db     61  FRAVTEITTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
Qy     121  ERGSYRYNFMNDGFLKVTVLSTFPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
Db     121  ERGSYTYNFMNDGFLKVTVLSTFPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
Qy     181  RDLVISISRDNTPALEPQPGNVPLYEAQKGQFLRLCAADSOPTATLSWLQNRVLSSS 240
Db     181  RDLVISISRDNTPALEPQPGNVPLYEAQKGQFLRLCAADSOPTATLSWLQNRVLSSS 240
Qy     241  HPWGPPLGLELPGVKAGSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVQANRTV 300
Db     241  HPWGPPLGLELPGVKAGSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVQANRTV 300
Qy     301  LENLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGQVLSQSPDGPVLELPRVQVE 360
Db     301  LENLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGQVLSQSPDGPVLELPRVQVE 360
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Qy      361  HEGFTTCHARHPLGSOHVLSLSLVHYSFKLLGSPSCSWEAEGHLHCSCSSQASPSPSLRWL 420
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Qy     421  GEELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCEAWNVHGAQSGSILQLP 480
Db     421  GEELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCEAWNVHGAQSGSILQLP 480
Qy     481  DKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQETPRPFRSRHSTILDYI 540
Db     481  DKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQETPRPFRSRHSTILDYI 540
Qy     541  NVVPTAGLAQKNQKATPNSPTPLPPGAPSPESKKNQKQYQLPSPFPKSKSTQAPES 600
Db     541  NVVPTAGLAQKNQKATPNSPTPLPPGAPSPESKKNQKQYQLPSPFPKSKSTQAPES 600
Qy     601  QESQELHYATLNFPGVRRPEARMKPGTQADYAEVKFQ 639
Db     601  QESQELHYATLNFPGVRRPEARMKPGTQADYAEVKFQ 639
Qy     639  QESQELHYATLNFPGVRRPEARMKPGTQADYAEVKFQ 677
Db     639  QESQELHYATLNFPGVRRPEARMKPGTQADYAEVKFQ 677
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Search completed: November 5, 2004, 14:13:49
Job time : 112.924 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:18 ; Search time 140.458 Seconds
(without alignments)
2617.614 Million cell updates/sec

Title: US-09-937-636-4
Perfect score: 3377
Sequence: 1 MLLPILLSLLGGSQAMDGR.....RPEARMPKGTADYAEVKFQ 639

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2790.5	82.6	544	2	Q6UXI8
3	2790.5	82.6	544	2	AAQ88703
4	2173	64.3	686	1	SILB_HUMAN
5	2108.5	62.4	425	2	BAC85493
6	1800	53.3	688	2	Q80ZE3
7	1668	49.4	623	2	Q8BY18
8	1047	31.0	551	1	SIL5_HUMAN
9	1039	30.8	551	2	AAH29896
10	837	24.8	569	1	SILF_MOUSE
11	772.5	22.9	523	2	Q80ZE2
12	721.5	21.4	499	1	SIL8_HUMAN
13	718.5	21.3	499	2	Q72728
14	700.5	20.7	595	1	SILL_HUMAN
15	692.5	20.5	597	1	SILL_PANTR
16	659.5	19.5	468	2	Q6PJ50
17	659.5	19.5	468	2	AAQ79834
18	659.5	19.5	468	2	AAQ72479
19	659.5	19.5	468	2	AAH23280
20	657.5	19.5	467	1	SIL5_MOUSE
21	640.5	19.0	463	1	SIL9_HUMAN
22	631.5	18.7	439	2	Q6GTU4
23	631	18.7	467	1	SIL7_HUMAN
24	620	18.4	394	2	Q6UXG0
25	620	18.4	394	2	AAQ88735
26	620	18.4	423	2	Q8BU57
27	607.5	18.0	442	1	SIL6_HUMAN
28	554.5	16.4	437	2	AAH35359
29	486	14.4	626	1	MAG_HUMAN
30	479	14.2	626	1	MAG_RAT
31	473	14.0	626	1	MAG_MOUSE

32 455.5 13.5 364 2 CAD36509
33 451.5 13.4 364 1 CD33_HUMAN
34 396 11.7 289 2 Q8BTG2
35 392 11.6 620 1 SMP_COTJA
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37 369.5 10.9 304 2 Q8IW38
38 368 10.9 233 2 AAS89010
39 368 10.9 403 1 CD33_MOUSE
40 367 10.9 233 2 AAS89009
41 361 10.7 233 2 AAS89011
42 337 10.0 269 2 Q95KP8
43 332 9.8 269 2 Q95KP9
44 332 9.8 271 2 Q95KQ0
45 311 9.2 852 1 CD22_MOUSE

ALIGNMENTS

RESULT 1

ID SILA_HUMAN STANDARD; PRT; 697 AA.
AC Q96LC7; Q96G54; Q96LC6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sialic acid binding Ig-like lectin 10 precursor (Siglec-10) (Siglec-like protein 2)
DE Name=SIGLEC10; Synonyms=SLG2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP MEDLINE=1303047; PubMed=11409878; DOI=10.1006/bhrc.2001.5053;
RA Yousef G.M., Ordon M.H., Fousias G., Diamandis E.P.;
RT "Molecular characterization, tissue expression, and mapping of a novel Siglec-like gene (SLG2) with three splice variants.";
RL Biochem. Biophys. Res. Commun. 284:900-910 (2001).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Spleen;
RX MEDLINE=21181594; PubMed=11284738;
RA Munday J., Kerr S., Ni J., Cornish A.L., Zhang J.Q., Nicoll G., Floyd H., Mattei M.-G., Moore P., Liu D., Crocker P.R.;
RT "Identification, characterization and leucocyte expression of Siglec-10, a novel human sialic acid-binding receptor.";
RL Biochem. J. 355:489-497 (2001).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Dendritic cell;
RX MEDLINE=21359381; PubMed=11358961; DOI=10.1074/jbc.M100467200;
RA Li N., Zhang W., Wan T., Zhang J., Chen T., Yu Y., Wang J., Cao X.;
RT "Cloning and characterization of Siglec-10, a novel sialic acid binding member of the Ig superfamily, from human dendritic cells.";
RL J. Biol. Chem. 276:28106-28112 (2001).
[4]
RN SEQUENCE FROM N.A. (ISOFORM 3), ALTERNATIVE SPLICING (ISOFORMS 4 AND 5), MUTAGENESIS OF TYR-667, AND INTERACTION WITH PTPN6.
RX MEDLINE=22152890; PubMed=12163025; DOI=10.1016/S0006-291X(02)00885-9;
RA Kitzig F., Martinez-Barriocanal A., Lopez-Botet M., Sayos J.;
RT "Cloning of two new splice variants of Siglec-10 and mapping of the interaction between Siglec-10 and SHP-1.";
RL Biochem. Biophys. Res. Commun. 296:355-362 (2002).
[5]
RN SEQUENCE OF 337-697 FROM N.A. (ISOFORM 1/3/4).
RC TISSUE=B-cell;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,

DR Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 DR Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
 DR Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 DR Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 DR Boak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 DR Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,
 DR Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 DR Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 DR Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 DR Blakeley R.W., Trichmond J.W., Green E.D., Dickson M.C.,
 DR Rodriguez A.C., Gilmour J.J., Schmutz J., Myers R.M.,
 DR Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalish D.E.,
 DR Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc Natl Acad Sci U S A. 99:16899-16903(2002).
 CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
 CC dependent binding to cells. Preferentially binds to alpha2,3- or
 CC 2,6-linked sialic acid. The sialic acid recognition site may be
 CC masked by cis interactions with sialic acids on the same cell
 CC surface. In the immune response, may act as an inhibitory receptor
 CC upon ligand induced tyrosine phosphorylation by recruiting
 CC cytoplasmic phosphatase(s) via their SH2 domain(s) that block
 CC signal transduction through dephosphorylation of signaling
 CC molecules.
 CC -!- SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1-4);
 CC secreted (isoform 5).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=Long;
 CC IsoId=Q96LC7-1; Sequences=Displayed;
 CC Name=2; Synonyms=Short, Sv1;
 CC IsoId=Q96LC7-2; Sequences=VSP_002565;
 CC Name=3; Synonyms=Sv3;
 CC IsoId=Q96LC7-3; Sequences=VSP_002564;
 CC Name=4; Synonyms=Sv4;
 CC IsoId=Q96LC7-4; Sequences=VSP_002561;
 CC Name=5; Synonyms=Sv2;
 CC IsoId=Q96LC7-5; Sequences=VSP_002563;
 CC TISSUE SPECIFICITY: Expressed by peripheral blood leukocytes
 CC (eosinophils, monocytes and a natural killer cell subpopulation).
 CC Isoform 5 is found to be the most abundant isoform. Found in lymph
 CC node, lung, ovary and appendix. Isoform 1 is found at high levels
 CC and isoform 2 at lower levels in bone marrow, spleen and spinal
 CC chord. Isoform 2 is also found in brain. Isoform 4 is specifically
 CC found in natural killer cells.
 CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
 CC as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
 CC motif is involved in modulation of cellular responses. The
 CC phosphorylated ITIM motif can bind the SH2 domain of several SH2-
 CC containing phosphatases.
 CC -!- PTM: Phosphorylation of Tyr-667 is involved in binding to PTPN6.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
 CC (sialic acid binding Ig-like lectin) family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AY029277; AAK40255.1; -
 CC EMBL: AY029277; AAK40256.1; -
 CC EMBL: AF310233; AAK55139.1; -
 CC EMBL: AF311905; AAK92542.1; -
 CC EMBL: AY032685; AAK51124.1; -
 CC EMBL: BC003955; AAK03955.2; -
 CC HSP: Q9Y286; 1C75. -

DR Genew: HGNC:15620; SIGLEC10.
 DR MIM: 606091; -
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00408; IG2; 2.
 DR PROSITE: PS00835; IG LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Alternative splicing; Cell adhesion; Glycoprotein;
 KW Immunoglobulin domain; Lectin; Phosphorylation; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 16 Potential.
 FT CHAIN 17 697 Sialic acid binding Ig-like lectin 10.
 FT DOMAIN 17 550 Extracellular (Potential).
 FT TRANSEM 551 571 Potential.
 FT DOMAIN 572 697 Cytoplasmic (Potential).
 FT DOMAIN 18 121 Ig-like V-type.
 FT DOMAIN 146 231 Ig-like C2-type 1.
 FT DOMAIN 251 339 Ig-like C2-type 2.
 FT DOMAIN 344 441 Ig-like C2-type 3.
 FT SITE 595 600 ITIM motif 1.
 FT SITE 665 670 ITIM motif 2.
 FT DISULFID 36 173 By similarity.
 FT DISULFID 41 101 By similarity.
 FT DISULFID 164 215 By similarity.
 FT DISULFID 276 323 By similarity.
 FT DISULFID 380 425 By similarity.
 FT MOD RES 667 667 Phosphotyrosine.
 FT CARBOHYD 100 100 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 364 364 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 486 486 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 504 504 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 125 214 Missing (in isoform 4).
 FT VARSPPLIC 140 185 Missing (in isoform 5).
 FT VARSPPLIC 186 697 Missing (in isoform 5).
 FT VARSPPLIC 141 198 Missing (in isoform 3).
 FT VARSPPLIC 445 539 Missing (in isoform 2).
 FT MUTAGEN 667 667 Y->F: Abolishes binding to PTPN6.
 FT CONFLICT 28 28 S -> P (in Ref. 4).
 FT CONFLICT 134 134 G -> R (in Ref. 4).
 FT CONFLICT 226 226 V -> A (in Ref. 1).
 FT CONFLICT 344 344 P -> S (in Ref. 3).
 FT CONFLICT 440 440 L -> P (in Ref. 4).
 FT CONFLICT 587 587 R -> K (in Ref. 3).
 FT CONFLICT 625 625 P -> S (in Ref. 3).
 SQ SEQUENCE 697 AA; 76619 MW; 6CB231CB49411D1B CRC64;
 Query Match 98.7%; Score 3334; DB 1; Length 697;
 Best Local Similarity 91.5%; Pred. No. 2.8e-202;
 Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;
 Qy 1 MLLPLLSLSLGGSQAMDGFRVIRVQESVYVMPGLCISVPCSFSPQDMGTGTPAYGYW 60
 Db 1 MLLPLLSLSLGGSQAMDGFRVIRVQESVYVMPGLCISVPCSFSPQDMGTGTPAYGYW 60
 Qy 61 FKAVTETTKGAPVATNHQREVEMSTRGRFQLTGDPKAGNCSLVIRDAQKQDESQYFFV 120
 Db 61 FKAVTETTKGAPVATNHQREVEMSTRGRFQLTGDPKAGNCSLVIRDAQKQDESQYFFV 120
 Qy 121 ERGSYVYVNFMDGFFLKVT-----VLSTPRQDHTDITCVHDFSRKGVSAQRTVRLRVAYAPRD 182
 Db 121 ERGSYVYVNFMDGFFLKVT-----VLSTPRQDHTDITCVHDFSRKGVSAQRTVRLRVAYAPRD 182

Db 181 TGAALSSQGTFTSHFSVFTFRPQDNDTDLCHVDVFSRKGVSQVTLRLVAYAPRD 240
Qy 183 LVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWVLQNRVLSSSH 242
Db 241 LVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWVLQNRVLSSSH 300
Qy 243 WGPRLGLGLPGVKAGDSGRYTCRAENLGSQORALDLSVOYPPENLRVMVSOANRTVLE 302
Db 301 WGPRLGLGLPGVKAGDSGRYTCRAENLGSQORALDLSVOYPPENLRVMVSOANRTVLE 360
Qy 303 NLNGNTSLPVLGGSLCLVCTHSSPPARLSTQRGQVLSQPSQSDPGVLELPRVQVEHE 362
Db 361 NLNGNTSLPVLGGSLCLVCTHSSPPARLSTQRGQVLSQPSQSDPGVLELPRVQVEHE 420
Qy 363 GEFTCHARHPLGSHVLSLSVHYSPKLLGPSCWEAEGHLCSSQASAPSLRWLWGE 422
Db 421 GEFTCHARHPLGSHVLSLSVHYSPKLLGPSCWEAEGHLCSSQASAPSLRWLWGE 480
Qy 423 ELLEGNSQSDSEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAMNVHGAQSGSILQLPDK 482
Db 481 ELLEGNSQSDSEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAMNVHGAQSGSILQLPDK 540
Qy 483 KGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRTQTETPRPFRSRHSTILDYINV 542
Db 541 KGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRTQTETPRPFRSRHSTILDYINV 600
Qy 543 VPTAGPLAQRNOKATNSPRTPLPGAPSPESKKNQKQYOLPSPFPKSTQAPESQ 602
Db 601 VPTAGPLAQRNOKATNSPRTPLPGAPSPESKKNQKQYOLPSPFPKSTQAPESQ 660
Qy 603 SOEELHYATLNFPGVVRPEARMKPGTQADYAEVKFQ 639
Db 661 SOEELHYATLNFPGVVRPEARMKPGTQADYAEVKFQ 697

DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 544 AA; 60267 MW; 4D4E1BFD60AC8CB CRC64;
Query Match 82.8%; Score 2790.5; DB 2; Length 544;
Best Local Similarity 84.8%; Pred. No. 4.4e-168;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;
Qy 1 MLLPLLLSSLLGSGQAMDGRFWIRVOESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Db 1 MLLPLLLSSLLGSGQAMDGRFWIRVOESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Qy 61 FKAVTTETTKGAPVATNHQSEVEMSTGRFQLTGDPAKGNCSLIVIRDAQMDSQFFRV 120
Db 61 FKAVTTETTKGAPVATNHQSEVEMSTGRFQLTGDPAKGNCSLIVIRDAQMDSQFFRV 120
Qy 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSRKGVSQVTLRLVAYAP 180
Db 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSRKGVSQVTLRLVAYAP 180
Qy 181 RDLVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWVLQNRVLSSSH 240
Db 181 RDLVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWVLQNRVLSSSH 240
Qy 241 HPKGPRLGLGLPGVKAGDSGRYTCRAENLGSQORALDLSVOYPPENLRVMVSOANRTV 300
Db 241 HPKGPRLGLGLPGVKAGDSGRYTCRAENLGSQORALDLSVOYPPENLRVMVSOANRTV 300
Qy 301 LENLNGTSLPVLGGSLCLVCTHSSPPARLSTQRGQVLSQPSQSDPGVLELPRVQVE 360
Db 301 LENLNGTSLPVLGGSLCLVCTHSSPPARLSTQRGQVLSQPSQSDPGVLELPRVQVE 360
Qy 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGPSCWEAEGHLCSSQASAPSLRWLW 420
Db 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGPSCWEAEGHLCSSQASAPSLRWLW 480
Qy 421 GEELEGNSSQSDSEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAMNVHGAQSGSILQLP 480
Db 387 ----- 386
Qy 481 DKGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRTQTETPRPFRSRHSTILDYI 540
Db 387 -KKGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRTQTETPRPFRSRHSTILDYI 445
Qy 541 NVPTAGPLAQRNOKATNSPRTPLPGAPSPESKKNQKQYOLPSPFPKSTQAPES 600
Db 446 NVPTAGPLAQRNOKATNSPRTPLPGAPSPESKKNQKQYOLPSPFPKSTQAPES 505
Qy 601 QESOBELHYATLNFPGVVRPEARMKPGTQADYAEVKFQ 639
Db 506 QESOBELHYATLNFPGVVRPEARMKPGTQADYAEVKFQ 544

RESULT 3
AAQ88703
ID AAQ88703 PRELIMINARY; PRT; 544 AA.
AC AAQ88703
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE SIGLEC10.
GN ORFNames=UNQ477;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358337; AAQ88703.1; -;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 2.

DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 544 AA; 60267 MW; 4D4E1BFD60AC8CB CRC64;
Query Match 82.8%; Score 2790.5; DB 2; Length 544;
Best Local Similarity 84.8%; Pred. No. 4.4e-168;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;
Qy 1 MLLPLLLSSLLGSGQAMDGRFWIRVOESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Db 1 MLLPLLLSSLLGSGQAMDGRFWIRVOESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Qy 61 FKAVTTETTKGAPVATNHQSEVEMSTGRFQLTGDPAKGNCSLIVIRDAQMDSQFFRV 120
Db 61 FKAVTTETTKGAPVATNHQSEVEMSTGRFQLTGDPAKGNCSLIVIRDAQMDSQFFRV 120
Qy 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSRKGVSQVTLRLVAYAP 180
Db 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSRKGVSQVTLRLVAYAP 180
Qy 181 RDLVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWVLQNRVLSSSH 240
Db 181 RDLVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWVLQNRVLSSSH 240
Qy 241 HPKGPRLGLGLPGVKAGDSGRYTCRAENLGSQORALDLSVOYPPENLRVMVSOANRTV 300
Db 241 HPKGPRLGLGLPGVKAGDSGRYTCRAENLGSQORALDLSVOYPPENLRVMVSOANRTV 300
Qy 301 LENLNGTSLPVLGGSLCLVCTHSSPPARLSTQRGQVLSQPSQSDPGVLELPRVQVE 360
Db 301 LENLNGTSLPVLGGSLCLVCTHSSPPARLSTQRGQVLSQPSQSDPGVLELPRVQVE 360
Qy 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGPSCWEAEGHLCSSQASAPSLRWLW 420
Db 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGPSCWEAEGHLCSSQASAPSLRWLW 480
Qy 421 GEELEGNSSQSDSEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAMNVHGAQSGSILQLP 480
Db 387 ----- 386
Qy 481 DKGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRTQTETPRPFRSRHSTILDYI 540
Db 387 -KKGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRTQTETPRPFRSRHSTILDYI 445
Qy 541 NVPTAGPLAQRNOKATNSPRTPLPGAPSPESKKNQKQYOLPSPFPKSTQAPES 600
Db 446 NVPTAGPLAQRNOKATNSPRTPLPGAPSPESKKNQKQYOLPSPFPKSTQAPES 505
Qy 601 QESOBELHYATLNFPGVVRPEARMKPGTQADYAEVKFQ 639
Db 506 QESOBELHYATLNFPGVVRPEARMKPGTQADYAEVKFQ 544

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
 Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 Godowski P.;
 "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 Bioinformatics Assessment.";
 Genome Res. 13:2265-2270(2003).
 EMBL; AY358337; AAQ88703.1; -
 NCBI TaxID=9606;
 SEQUENCE 544 AA; 60267 MW; 4DA4E1EFD60AC8B CRC64;
 Query Match 82.6%; Score 2790.5; DB 2; Length 544;
 Best Local Similarity 84.8%; Pred. No. 4.4e-168;
 Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;
 QY 1 MLPLLLSSLLGGSQANDGRFWIRVOESVMVPEGLCISVPCFSYPRQDWTGTPAYGYW 60
 DB 1 MLPLLLSSLLGGSQANDGRFWIRVOESVMVPEGLCISVPCFSYPRQDWTGTPAYGYW 60
 QY 61 FKAVTTTKAPVATNHQSEVEMSTRGRFQLTGDPAKNGCSIVTDAQMDQESQYFRV 120
 DB 61 FKAVTTTKAPVATNHQSEVEMSTRGRFQLTGDPAKNGCSIVTDAQMDQESQYFRV 120
 QY 121 ERGSYVYNPMNDGFFLKVTLSFTPRPDQNTDLTCHVDTSRKGVSQAQTVRLVAVAP 180
 DB 121 ERGSYVYNPMNDGFFLKVTLSFTPRPDQNTDLTCHVDTSRKGVSQAQTVRLVAVAP 180
 QY 181 RLIVISIRNDTALPPOGQNVPLYEAQGFQLRLCAADQPATLSWLVQNRVLSS 240
 DB 181 RLIVISIRNDTALPPOGQNVPLYEAQGFQLRLCAADQPATLSWLVQNRVLSS 240
 QY 241 HPWGPRLGLPLGVKAGDSGRVTCRAENRLGSGQBALDLSVQYPPENLRVMVQANRTV 300
 DB 241 HPWGPRLGLPLGVKAGDSGRVTCRAENRLGSGQBALDLSVQYPPENLRVMVQANRTV 300
 QY 301 LENLNGTSLPVLEGQSLVCVTHSGPPARLSWTORGQVLSQSPSDGVLRLRVQVE 360
 DB 301 LENLNGTSLPVLEGQSLVCVTHSGPPARLSWTORGQVLSQSPSDGVLRLRVQVE 360
 QY 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGPSCSWEAEGHLCSSQASAPSLRWL 420
 DB 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGPSCSWEAEGHLCSSQASAPSLRWL 420
 QY 421 GEBLEGNSSQDSFEVTPSSAGFWANSSLSLHGLSSGLRLCEANVHGAQSGSILQJP 480
 DB 387 ----- 386
 QY 481 DKGLISTAFSGAFIGIGITALLFLCLALITKILPKRTOTETPRFSSHSTILDYI 540
 DB 387 -XKGLISTAFSGAFIGIGITALLFLCLALITKILPKRTOTETPRFSSHSTILDYI 445
 QY 541 NVVPTAGPLAQRNOKATNSPRTPPPGAPSPESKQKQYQLPSPPEKSSQAPES 600
 DB 446 NVVPTAGPLAQRNOKATNSPRTPPPGAPSPESKQKQYQLPSPPEKSSQAPES 505
 QY 601 QESQELHYATLNFQVRPRPAPKPGTQADYAEVKFQ 639
 DB 506 QESQELHYATLNFQVRPRPAPKPGTQADYAEVKFQ 544

RESULT 4

ID SILB HUMAN STANDARD; PRT; 686 AA.
 AC Q96RL6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sialic acid binding Ig-like lectin 11 precursor (Siglec-11) (Sialic
 acid-binding lectin 11) (UNQ9222/PRO28719).
 GN Name=SIGLEC11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI TaxID=9606;
 [1]
 RX SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH PTPN6 AND PTPN11.
 RP MEDLINE=22086217; PubMed=11986327; DOI=10.1074/jbc.M202833200;
 RA Angata T., Kerr S.C., Greaves D.R., Varki N.M., Crocker P.R.,
 Varki A.;
 "Cloning and characterization of human Siglec-11. A recently evolved
 signaling that can interact with SHP-1 and SHP-2 and is expressed by
 tissue macrophages, including brain microglia.";
 J. Biol. Chem. 277:24466-24474(2002).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
 Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 Godowski P., Gray A.;
 "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 Genome Res. 13:2265-2270(2003).
 CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
 dependent binding to cells. Preferentially binds to alpha2,8-
 linked sialic acid. The sialic acid recognition site may be masked
 by cis interactions with sialic acids on the same cell surface. In
 the immune response, may act as an inhibitory receptor upon ligand
 induced tyrosine phosphorylation by recruiting cytoplasmic
 phosphatase(s) via their SH2 domain(s) that block signal
 transduction through dephosphorylation of signaling molecules.
 CC -!- SUBUNIT: Interacts with PTPN6/SHP-1 and PTPN11/SHP-2 upon
 phosphorylation.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Name=1;
 IsoId=Q96RL6-1; Sequence=Displayed;
 Name=2;
 IsoId=Q96RL6-2; Sequence=VSP_008764;
 CC -!- TISSUE SPECIFICITY: Expressed by macrophages in various tissues
 including Kupffer cells. Also found in brain microglia.
 CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
 as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
 motif is involved in modulation of cellular responses. The
 phosphorylated ITIM motif can bind the SH2 domain of several SH2-
 containing phosphatases.
 CC -!- PTM: Phosphorylated on tyrosine residues.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
 (sialic acid binding Ig-like lectin) family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -----
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 or send an email to license@isb-sib.ch).

 EMBL; AF337818; AAQ72907.1; -
 EMBL; AY358135; AAQ88502.1; -
 HSP; Q9V286; 1078.
 Genew; HGNC:15622; SIGLEC11.
 MIM; 607157; -
 InterPro; IPR007110; Ig-like.
 InterPro; IPR003006; Ig_MHC.
 Pfam; PF00047; Ig; 3.

DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; 1.
KW Alternative splicing; Cell adhesion; Glycoprotein;
KW Immunoglobulin domain; Lectin; Phosphorylation; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 15 Potential.
FT CHAIN 16 686 Sialic acid binding Ig-like lectin 11.
FT DOMAIN 16 549 Extracellular (Potential).
FT TRANSMEM 550 572 Potential.
FT DOMAIN 573 686 Cytoplasmic (Potential).
FT DOMAIN 19 122 Ig-like V-type.
FT DOMAIN 147 232 Ig-like C2-type 1.
FT DOMAIN 229 338 Ig-like C2-type 2.
FT DOMAIN 343 440 Ig-like C2-type 3.
FT SITE 630 635 ITIM motif.
FT DISULFID 37 174 By similarity.
FT DISULFID 42 102 By similarity.
FT DISULFID 165 216 By similarity.
FT DISULFID 275 322 By similarity.
FT DISULFID 379 424 By similarity.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 250 250 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 354 354 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 363 363 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 485 485 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 503 503 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 443 539 YPQLLPSCWEAEGLHCSCSSQASPAPSLRWLGEELLE
GNSQGSFEVTPSSAGPWANSLSLHGGSSGLRLRCKAWN
VFGAQSQSVFQLLP -> W (in isoform 2).
/FTID=VSP_008764.
FT CONFLICT 84 84 E -> A (in Ref. 2).
FT CONFLICT 353 353 A -> G (in Ref. 2).
FT SEQUENCE 686 AA; 74544 MW; FDEAI193615685A8 CRC64;
Query Match 64.3%; Score 2173; DB 1; Length 686;
Best Local Similarity 63.3%; Pred. No. 6.2e-129;
Matches 440; Conservative 50; Mismatches 111; Indels 94; Gaps 6;
QY 1 MLPLILLSLGGSQAMDGRFWRVQESVMVEGLCISVPCSFSPYPRQDWTGSTPAYGVW 60
DB 2 LLLPLLPVLGSLNKPDSYLVQVRQVPVEGLCVISCNLSYPRGDWDESTAYGVW 61
QY 61 FRAVTEETTKGAPVATNHQREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESYFFRV 120
DB 62 FGRTSPKTPGAPVATNHQREVEMSTRDRFQLTGDPKAGNCSLVIRDAQREDEMYFFRV 121
QY 121 ERGSYVRYNFMNDGPFILKT----- 140
DB 122 ERGSVRHSFLSNAPFLKVTALTAKPDVYIPETLEFGQPVTVICVFNWAFKCKPAPFSW 181
QY 141 -----VLSPTRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPED 182
DB 182 TGAALSPRTRSTSHFSVLSFTPSQDHDHDLTCHVDFSRKGVSAQRTVRLRVAYAPKD 241
QY 183 LVTSISRDNTPALEPOQGNVPYLEAKQGFRLLLCAADSQPPATLSWYLNQVLSSSH 242
DB 242 LAISISHDNTSALE--LQGNVYILEYKQGFRLLLCAADSQPPATLSWYLNQVLSSSH 299
QY 243 WGRPPLGLELPVKGAGDGRYTCRAENRLGSOORALDLSVOYPPENLRVMVQANRTVLE 302
DB 300 WGRPTLGLRUGRAGDSGRYTCRAENRLGSOOQALDLSVQYPPENLRVMVQANRTVLE 359
QY 303 NLNGTSLPYLEGQSCLVCVTHSSPPARLSWTQGVLSPSQSPDPGVLELPVQVEHE 362
DB 360 NLNGTSLPYLEGQSCLRLVCVTHSSPPARLSWTQGVLSPSQSPDPGVLELPVQMEHE 419
QY 363 GEFTCHARHPLGSHVLSLSVHYSPKLLGPSCSWEAEGHLHCSCSSQASPAPSLRWLGE 422
DB 420 GEFTCHARHPLGSHVLSLSVHYSPKLLGPSCSWEAEGHLHCSCSSQASPAPSLRWLGE 479
QY 423 ELLEGNSQDSFEVTPSSAGPWANSLSLHGGSSGLRLRCKAWNVEHGAQSIIQLPDK 482

DB 480 ELLEGNSQDSFEVTPSSAGPWANSLSLHGGSSGLRLRCKAWNVEHGAQSIVFQLLP 539
QY 483 KGLISTAFSNGAFILGIGITALLFLCLALIMKILPKRTOTETPRPRFSRHSTILDYINV 542
DB 540 KLEHGGGLGLGAALGAGVAALLAFCSCLVVRVKICRK-----EARKFAAAEQ-----DV 589
QY 543 VPTRAGPLAOKENOKATPNSPRTPLPGCAPSPESKCKQKQYQLPSPPEKSSVTCAPESQE 602
DB 590 PSTLGPISQGHQHECSAGSSQDHPPPGA-----AYTPKGE 626
QY 603 SQBELHYATLNFPGVRPRPEARMKPGTQADYAEVK 637
DB 627 EQ-ELHYASLSFQGLRLWEPAQOEAPSTTEYSBIK 660
RESULT 5
BAC85493
ID BAC85493 PRELIMINARY; PRT; 425 AA.
AC BAC85493;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE CDNA FLJ16033 fis, clone SPLEN2001599, weakly similar to Homo sapiens
DE sialic acid binding immunoglobulin-like lectin 8 long splice variant
DE (Siglec8) gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RA "NEDO human cDNA sequencing project";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK122619; BAC85493.1; -.
KW Lectin.
SQ SEQUENCE 425 AA; 47345 MW; 809854127B397D73 CRC64;
Query Match 62.4%; Score 2108.5; DB 2; Length 425;
Best Local Similarity 69.0%; Pred. No. 4e-125;
Matches 421; Conservative 1; Mismatches 3; Indels 185; Gaps 2;

QY 30 MVPEGLCISVPCSFSPYPRQDWTGSTPAYGVWFKAVTETTKGAPVATNHQREVEMSTRGR 89
DB 1 MVPEGLCISVPCSFSPYPRQDWTGSTPAYGVWFKAVTETTKGAPVATNHQREVEMSTRGR 60
QY 90 FOLTGDPKAGNCSLVIRDAQMDQESYFFRVGRSVRYNFMNDGFFLKVTLSFTPRQ 149
DB 61 FOLTGDPKAGNCSLVIRDAQMDQESYFFRVGRSVRYNFMNDGFFLKVTLSFTPRQ 120
QY 150 DHNTDLTCHVDVFSRKGVSQRTVRLRVAYAPRDLVISISRDNTPALEPQPGQGNVPYLEAQ 209
DB 121 DHNTDLTCHVDVFSRKGVSQRTVRLRVAYAPRDLVISISRDNTPD----- 165
QY 210 KGQFRLLLCAADSQPPATLSWYLNQVLSSSHPPGRLGLELPGVKAGDSGRYTCRAEN 269
DB 166 ----- 165
QY 270 RLGSQORALDLSVOYPPENLRVMVQANRTVLENLNGTSLPYLEGQSCLVCVTHSSPP 329
DB 166 -----PENLRVMVQANRTVLENLNGTSLPYLEGQSCLVCVTHSSPP 210
QY 330 ARLSWTQGVLSPSQSPDPGVLELPVQVEHEGEFTCHARHPLGSHVLSLSVHYSPK 389
DB 211 ARLSWTQGVLSPSQSPDPGVLELPVQVEHEGEFTCHARHPLGSHVLSLSVHYSPK 267


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QY 390 LLGPSCSWEAEGHLHCSCSSQASPAPSLRWMLGELLGNSSQDSFVTPSSAGPWANSSL 449
DB 268 ----- 267
QY 450 SLHGLSSGLRLRCEANVHGAOSGSLQDPKKGLISTAFNSGAFLGITALLFLCLA 509
DB 268 -----KKGLISTAFNSGAFLGITALLFLCLA 295
QY 510 LIIMKILPKRTOTETPRPFSRHSHTLDYINVVPTAGPLAOKRNOKATPNSPRTPLPG 569
DB 296 LIIMKILPKRTOTETPRPFSRHSHTLDYINVVPTAGPLVQKRNOKATPSSPRTPLPG 355
QY 570 APSPEKKNKKQYQLPSPFPPEKSSSTQAPESQBSQELHYATLNFPGVPRPEARMKGT 629
DB 356 APSPEKKNKKQYQLPSPFPPEKSSSTQAPESQBSQELHYATLNFPGVPRPEARMKGT 415
QY 630 QADYAEVKFQ 639
DB 416 QADYAEVKFQ 425

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RESULT 6

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#Q80ZE3 ID Q80ZE3 PRELIMINARY; PRT; 688 AA.
AC Q80ZE3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DI 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Siglec-G.
GN Name=Siglec10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RV MEDLINE=22921108; PubMed=14559209;
WA Aizawa H., Zimmermann N., Carrigan P.E., Lee J.J., Rothenberg M.E.,
RT "Molecular analysis of human Siglec-8 orthologs relevant to mouse
RT eosinophils: identification of mouse orthologs of Siglec-5 (mSiglec-F)
RT and Siglec-10 (mSiglec-G).";
RN Genomics 82:521-530(2003).
DR EMBL; AY210400; AAC48273.1; -.
DR HSSP; Q9Y286; I07S.
DR MGD; MGI:2443630; Siglec10.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 688 AA; 76884 MW; 21A619B1500BFA76 CRC64;

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Query Match

Best Local Similarity 54.9%; Pred. No. 2.3e-105; Length 688;

Matches 381; Conservative 70; Mismatches 175; Indels 68; Gaps 9;

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QY 2 LPLLLSSLLGSSQMDGRFWTRVQESVWVPEGLICISVPCSPSYPRQDWTGSTAYGWYF 61
DB 3 LLLFLSLFLDLPQGGMESYFLQVQRIKVAQEGLCIFVPCSPSPSGKWLNRSELYGYWF 62
QY 62 KAVTETTKGAPVATNHSREVMSTRGRFQLTGDPAKNCSLVIRDAQWQESQVFFRVE 121
DB 63 KGIRKPSLSFPVATNNKVKLWEARGFQLLGDSIKKNCILLIKDVGWGSTNYFFRME 122
QY 122 RGSYVRYNFMN-----DGFPLKY----- 139
DB 123 RG-FRFFSPKFRILQVEALTKQDIFPEVLEPGEPVTVVCLFSWTFNQCPAPSFWSMG 181
QY 140 -----TVLSFTFRPDNDTDLTCHVDFSRKGVSAQRTVRLRVAVAPRDLV 184

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DB 182 DAVSFQESRPHTSNYSVLSPFPGQLQHDHDTLTQLDFTSR--MSTQRTVRLRVAVAPRSLA 239
QY 185 ISIREDNTPALEPOQGNVPYLEAKQGFIRLLCAADSOPATLSWTLQNRVLSSHPWG 244
DB 240 ISIFDHNVSV--PDHENPSSHLEVQCGQSRLKLTADSQPPATLSWLEVDQVLSWSVPVG 297
QY 245 PRPLGLEPGVKAGDSGRYTCRAENRLGSGQORA.DLSVQYFPPENLRVWVQANRTVLENL 304
DB 298 SRTLALSLPWYKAGDSGHYTCQENRLGSGQHTLDLSVLYPQDLRTVQANRTVLEIL 357
QY 305 GNGTSLPVLBQSLCLVCVTHSSPPARLSWTQGVLSPPQSDPGVLELPRVQVHEGE 364
DB 358 RNAISLPLVLEBQSLCLVCVTPNSPPANVSWAWVTQTLPICSSSEPGVLELPLVQREHEGE 417
QY 365 FTCHARPLGSHVSLSVHYSPLKLGPCSWAEGLHCSCSSQASPPASLRWMLGEEL 424
DB 418 FTCAQNPGLQARISLSLVHYPQMSPPSCSWEAKGLHCNCSSRAWPAFLRWLGEGL 477
QY 425 LEGNSSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCEANVHGAOSGSLIQLPKKG 484
DB 478 LEGNSSNASFTVTFSSSLGPPWVNSLSLLQELGSLMLSCSWNTHGAQTTSVLLLPKOKS 537
QY 485 LISTAFSNGAFLGITALLFLCLALIIIMKILPKRRTQTETPRFSRHSHTLDYINVP 544
DB 538 --ATAFSKGAVLGFIITALLALCLIVIVITLQKGTQEPSPKLSRGSTILDYINVP 595
QY 545 TAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNQK-KOYQLSPFPPEPKSSTQAPESQES 603
DB 596 KTRSLA--RWKAEPDAPSSSSPLDTHFPKPKKQKDPHTTYPGCPDPTSSSQVPVSENN 653
QY 604 QEELHYATLNPFGVPRPEARMKPGTQADYAEVK 637
DB 654 PEELHYAALNPSRLRLQ-ETQDPQTYSDYTEVR 686

```

RESULT 7

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Q8BY18 ID Q8BY18 PRELIMINARY; PRT; 623 AA.
AC Q8BY18;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DI 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630096C01 product:weakly similar to SIALLIC ACID-
DE BINDING LECTIN (Fragment).
GN Name=Siglec10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RV MEDLINE=99279253; PubMed=10349636;
WA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RN Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RV MEDLINE=21085660; PubMed=11217851;
WA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RV MEDLINE=21085660; PubMed=11217851;
WA RIKEN FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RN Nature 420:563-573(2002).
RN [4]

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RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076961;
RA Shibata K., Itoh M., Aizawa K., Katsunai T., Tashiro H., Itoh M.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Onodera Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "Riken integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK042488; BAC31272.1; -
DR HSSP; Q9Y286; 107S.
DR MGD; MGI:2443630; Siglec10.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG1.2.
DR SMART; SM00408; IGc2.2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Lectin.
FT NON_TER
SQ SEQUENCE 623 AA; 59384 MW; 5827C09D52C3AC7F CRC64;
Query Match 49.4%; Score 1668; DB 2; Length 623;
Best Local Similarity 56.3%; Pred. No. 4.4e-97;
Matches 351; Conservative 58; Mismatches 148; Indels 66; Gaps 7;
QY 2 LPLLLSLLGSGQAMDRFWIRVOESVMVEGLICISVPCSPSPRODWTGSTAYGYWF 61
DB 3 LLLFLSLFDLPQOMSESYFLQVRIYKAOEGLCIFVPCSPSPGKWLNRSLPYGYWF 62
QY 62 KAVTETTKGAPVATNHQREVEMSRGRFQLTGDPKAGNCISIVIRDAQKQDESQVFFRVE 121
DB 63 KGIRKPSLSPFVATNKKVLEWEARGFQLLDGDISKNCNLLIKDVQWGSDTVYFFRME 122
QY 122 RGSYVRYFMN-----DGFLLKY----- 139
DB 123 RG-FERFSGKBEFLRLQVEALTKPDIFIPVLEPGEPVTVVCLFSWTFNQCPAFSFMWG 181
QY 140 -----TVLSFTFRPDHNTDLCHVDKSGVSAQRTVLRVAVAPRLV 184
DB 182 DAVSQESRPTNSVSLVSIFGLQHHDTLTCQLDFSR--MSTQRTVLRVAVAPRLA 239
QY 185 ISISRNTPALPFPQGNVPYLEAQKQFLRLCAADSQPPATLSVQLQNRVLSSHPWG 244

DB 240 ISIFHDNVSV--PDHFNPSHLEVQQQSLRLCTADSQPPATLSVWLEQVLSWSSPVG 297
QY 245 PRPLGLELPQVKGADSGRTCTRAENRLGSGQALDLSVQVPPENLRVMVSQANRTVLENL 304
DB 298 SRTLALELPVWKGADSGHYTCQANRLGSGQHTLDLSVLYPPQDLRTVTSQANRTVLEIL 357
QY 305 GNGTSLPVLREGQSLCLVCTVTHSSPPARLSWTQSGVLSPSQSPDPGVLELPRYQVREHE 364
DB 358 RNAISLPVLEGGQSLCLVCTVTSNPPANVSNWAWTQTLPIQSEPGVLELPLVQREHEGE 417
QY 365 FTCHARHPLGSHVSLSLSVHSPKLLGLPSCSWAEAGLHCSCSSQASPPAPSLRWLGEEL 424
DB 418 FTCAAQNPGLGAQRISLSLSLVHPYQMSPPSCSWAEAGLHCNCSSRAWPAPSLRWLGEGL 477
QY 425 LEGNSSODSPETVPSSAGPWANSSLSHGLSSGLRLCRBAMNVHGAQSGSIIQLDPKKG 484
DB 478 LEGNSSASVTTFSSLGPWVNSLSLLQLGLPSLWLSCESWNTHGAQTTSVLLLPDKDS 537
QY 485 LISTAFSNGAFLGIGITALLFLCLALIMKLPKRTQTETPRFRSRHSTILDYINVP 544
DB 538 --ATARSGAVLGFGITALLALCLIVIVKTLQKGTQEBSPKLSRGSTILDYINVP 595
QY 545 TAGPLAQXRNQKATPNSPRTPLP 567
DB 596 KTRSLA--RNWKAEPDAPSRSSP 616
RESULT 8
SILS_HUMAN
ID -SILS_HUMAN STANDARD; PRT; 551 AA.
AC O15389;
DT 28-FEB-2003 (Rel. 41, Created)
DD 28-FEB-2003 (Rel. 41, Last sequence update)
DI 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sialic acid binding Ig-like lectin 5 precursor (Siglec-5) (Obesity-
DE binding protein 2) (OB binding protein-2) (OB-BP2) (CD33 antigen-like
DE 2) (CD170 antigen).
GN Name:SIGLECS; Synonyms:OBBP2, CD33L2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX MEDLINE=98402360; PubMed=9731071;
RA Cornish A.L., Freeman S., Forbes G., Ni J., Zhang M., Cepeda M.,
RA Gentz R., Augustus M., Carter K.C., Crocker P.R.;
RT "Characterization of siglec-5, a novel glycoprotein expressed on
RT myeloid cells related to CD33.";
RL Blood 92:2123-2132(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Erythrocytosis;
RX MEDLINE=9357812; PubMed=10428856;
RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
RA Varki A., Kastelein R.A.;
RT "OB-BP1/Siglec-6: A lepton-and sialic acid-binding protein of the
RT immunoglobulin superfamily.";
RL J. Biol. Chem. 274:22729-22738(1999).
RN [3]
RP ERRATUM.
RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
RA Varki A., Kastelein R.A.;
RL J. Biol. Chem. 274:28058-28058(1999).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lander J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,

Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M., Cleland C.A., Copeland A., Dain E., Dehal P., Denys M., Dettler J.C., Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M., Glavina T., Gomez M., Gonzales E., Groza M., Hamon N., Hawkins T., Haydu L., Ho I., Huang W., Israni S., Jet J., Kadner K., Kimball H., Kobayashi A., Lartionov V., Leem S.-H., Lopez F., Lou Y., Lowry S., Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J., Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M., Popkie A.P., Predki P., Quan G., Ramirez L., Raeh S., Retterer J., Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D., Slezak T., Solovayev V., Thayer N., Tice H., Tsai M., Ustaszewska A., Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I., Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.B., Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M., Rubin E.M., Lucas S.M., "The DNA sequence and biology of human chromosome 19"; Nature 428:529-535(2004).

-1- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Binds equally to alpha2,3-linked and alpha2,6-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- TISSUE SPECIFICITY: Expressed by monocytic/myeloid lineage cells. Found at high levels in peripheral blood leukocytes, spleen, bone marrow and at lower levels in lymph node, lung, appendix, placenta, pancreas and thymus. Expressed by monocytes and neutrophils but absent from leukemic cell lines representing early stages of myelomonocytic differentiation.

-1- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.

-1- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-like lectin) family.

-1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

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EMBL; AF170484; RAD50978.1; -
EMBL; U71383; AAF70703.1; -
EMBL; AC018755; AAF87846.1; -
HSSP; Q9Y286; 107S.
GeneID; HGNC:10874; SIGLEC5.
MIM; 604200; -
InterPro; IP3007110; Ig-like.
InterPro; IP3003598; Ig_c2.
InterPro; IP3003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 3.
Antigen; Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Polymorphism; Repeat; Signal; Transmembrane.
SIGNAL 1 16 Potential.
FT CHAIN 17 551 Sialic acid binding Ig-like lectin 5.
FT DOMAIN 17 441 Extracellular (Potential).
FT TRANSMEM 442 462 Potential.
FT DOMAIN 463 551 Cytoplasmic (Potential).
FT DOMAIN 19 136 Ig-like V-type.
FT DOMAIN 146 228 Ig-like C2-type 1.
FT DOMAIN 236 330 Ig-like C2-type 2.
FT SITE 518 523 ITIM motif.
FT SITE 542 523 SLAM-LIKE MOTIF.
FT DISULFID 36 170 By similarity.

FT DISULFID 41 101 By similarity.
FT DISULFID 164 213 By similarity.
FT DISULFID 269 314 By similarity.
FT CARBOHYD 100 100 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 210 210 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 231 231 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 253 253 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 328 328 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 375 375 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 384 384 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).
FT VARIANT 72 72 V -> A (in dbSNP:1973019).
FT VARIANT 215 215 M -> V (in dbSNP:1807124).
FT VARIANT 322 322 P -> S (in dbSNP:2278831).
FT CONFLICT 309 309 E -> K (in Ref. 1).
FT CONFLICT 358 358 R -> W (in Ref. 1).
FT CONFLICT 388 388 A -> P (in Ref. 1).
FT CONFLICT 403 403 S -> N (in Ref. 1).
SQ SEQUENCE 551 AA; 60715 MW; 2FEA2B6B341EPEAF CRC64;
Query Match 31.0%; Score 1047; DB 1; Length 551;
Best Local Similarity 39.4%; Pred. No. 6.6e-58;
Matches 256; Conservative 76; Mismatches 203; Indels 114; Gaps 15;
Oy 2 LPLLLSLG-GSQAMDGFWRVQESVNVVPGLCISVPCSFSPRODWTGTTPAYGW 60
Db 1 MLPULLPLWGLGSLQKPYELQVQKSVTVQGLCVLPSCSFSPWRSWYSEPLVYW 60
Oy 61 FKAVTETKGAIVATNQHSREVMSTRGFLQTDGPAKNCISVIRDAQMDQSDQFFRV 120
Db 61 FRDGEIPYAEVAVATNPNDRVRKPTQGRRLGLDGVQKNCISIGDARMEDTGSYFFRV 120
Oy 121 ERGSYVYFNPMNDGFLKVTVLSTFPQPDHNDLICHVDVFSRKGVSQAQTVRLVAYAP 180
Db 121 ERGRDVKYSQOKNLEVTAL----- 142
Oy 181 RDLVISRDNTPALEPQPGNVPLYEAQKQFLRLLC-----AASQPPATLSWVLQNRV 236
Db 143 -----LEKEDIHFLEP-----LESGRFRLSCSLPGSCAAGPLTFST--GNA 184
Oy 237 LSSSHPMGPRPLGLELPGVVAGSGRYTCRAENRGSQ---QALDLSVQYPPENLRVMV 293
Db 185 LSPLEDPETTRSSSLTTPRPEDHGTNLTCOMK-ROGAQVTTERTVQLNVSYADPTITIF- 242
Oy 294 SQANRTVLENLGNGTSLPVLEGOSLCIVCVTHSSPPARLSWTQGVLSQSPQDPGVLE 353
Db 243 --RNGIALEILQNTSYLPVLEGALRLLCDPSPNPAHLNFWFGSPALNATPISNTGILE 300
Oy 354 LPRVQVEHEGEPTCHAKHPVLSQHSVLSUSVHYSPKLLGPSCSWAEGLHCSCSSQASPA 413
Db 301 LRRVRSABEGGFTCRAGHPGLFLQIFNLNVSVGLPQLLGPSCSWAEGLHCRCSTFARPA 360
Oy 414 PSLRWMLGELLNCSQDSFEVTPPSAGPWNSSLSHGLSGSLRCEANNVHGAQS 473
Db 361 PSCWRLEKPLEGNSQSGFKVNSSAGPWNSSLLHGLSSDLKVCSSKANNVYGSQS 420
Oy 474 GSIIQLPDKKGLISTAFNSGAFILGIGITALLFLCLALIMKILPKRTQTETPRPFRSH 533
Db 421 GSVLLQGRSNL-CTGVVPAALGGAGVMALLCICLIFFLIVKARRKQA-AGRPEKMD 478
Oy 534 STLDYINVVPTAGPLACKNOKATPNSRTPPL-PPGAPSPESKKNQKQYQLPSPEPK 592
Db 479 ED-----PIMGTTTSGRKKPWPDPSPQDSQSPGDAPP----- 511
Oy 593 SSTQAPESQESQELHVAIVNFQGVPRPRPEARMKGTQA----DYAEVK 637
Db 512 -----LEEQKELHVASISFSEMK-----SREPKQEAAPTTEYSEIK 548

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AAH29896
ID AAH29896 PRELIMINARY; PRT; 551 AA.
AC AAH29896;
DT 02-MAR-2004 (TRENDELrel. 27, Created)
DT 02-MAR-2004 (TRENDELrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENDELrel. 27, Last annotation update)
DE Sialic acid binding Ig-like lectin 5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.J., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Krausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029896; AAH29896.1; .
KW Lectin
SQ SEQUENCE 551 AA; 6068 MW; 65EA2B6B29B59304 CRC64;

Query Match 30.8%; Score 1039; DB 2; Length 551;
Best Local Similarity 39.3%; Pred. No. 2.1e-57;
Matches 255; Conservative 76; Mismatches 204; Indels 114; Gaps 15;

QY 2 LPLLLSL-CGSOAMDGRFWRVOESVMYVEGLCISVPCSFSPRODWTGSGTPAYGW 60
DB 1 MLPLLLPLLLWGGSLQKXPVYELQVQKSVTVQEGLCVLVPCSFSPWRSWYSSPLYYW 60
QY 61 FRAVTEETTKGAPVATNHOSREVEMSTRGRFQLTGDPKXGNSLVLRDAQMODESOYFFRV 120
DB 61 FRDGEIPYAEVVAATNPDRVRKPTQGRFLLGDVQKNCSLSDGARMEDTGSYFFRV 120
QY 121 ERGSVYRNFMDGFLKVTLSFTFRPODNDTLTCHVDFSRKGVSAQRTVRLVAVAP 180
DB 121 ERGRDVKSYYQOKNLNLEVTAL----- 142
QY 181 RDLVTSISRDNTFALEPOGPNVPLEAKGQFRLLC-----AADSQPPATLSWVLQNRV 236
DB 143 -----LEKPDHFLFEP-----LESGPTRLSCSLPGSCAGPLFTFSWT--GNA 184
QY 237 LSSHPWGPRLPLGLPGVKAQSGRYTCRAENLGSQ---ORALDLSVQVPPENLVMV 293
DB 185 LSPLDPEPTRSSSELTLPPEDHGNTLTCQMK-RQCAQVTTERTVQLNVSVAPQTITIF- 242
QY 294 SOANRTVLENLNGSLPLVLEQSSCLVCTHSSPPARLSWTQGVLSPOSPDPGVLE 353
DB 243 --RNGIALEILQNTSVLPVLEQARLLCDAPSNFAHLSWFGQSPALNATPISNTGLE 300
QY 354 LPRVQVEHEGEFTCHARHPLGSGVHVSLSLSVHSPKLLGSPCSWEAEGHLHCSCSQASPA 413
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Db 301 LRRVSAEAGGFTCRAQHPLGFLQIFLNLSVYSLPQLLGPSCSWAEAGLHCRCSPRAPA 360
QY 414 PSRLWMLGEBELLEGNSSQSFVTPSSAGPWNSSLSLHGLSSGLRLRCRANVHGAQS 473
Db 361 PSLCWRLEEKPLEGNSSQSFVKYNSSAGPWNSSLSLHGLSSGLKVKSCKANIYGSQS 420
QY 474 GSILQLPDKKGLISTAFSNGAPLIGITALLFCLALIMKILPKRRTOTETPRPRFSRH 533
Db 421 GSVLLQGRNL-GTGVVPAALGAGVWALLCICLIFLIYKARKQA-AGRPKQMD 478
QY 534 STILDYINVVPTAGPLAQKRNKATNSPTPL-PPGAPSPESKKNQKQYQLPSPPEPK 592
Db 479 ED-----PINGTTTSGSRKPPWDSAGDQASPPGDAPP----- 511
QY 593 SSTQAPESQESQELHYATLNFQVPRPEARMKCTQA-----DYAEVK 637
Db 512 -----LEEQKELHYASLFSSEMK-----SRFQKQEAAPTTEYSEIK 548

RESULT 10
SILF MOUSE
ID -SILF_MOUSE STANDARD; PRT; 569 AA.
AC Q920G3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sialic acid binding Ig-like lectin-F precursor (mSiglec-F).
GN Name=SiglecF, (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA MEDLINE=21576254; PubMed=11579105; DOI=10.1074/jbc.M108573200;
RA Angata T., Hingorani R., Varki N.M., Varki A.;
RT "Cloning and characterization of a novel mouse Siglec, mSiglec-F:
RT differential evolution of the mouse and human (CD33) Siglec-3-related
RT gene clusters.";
RL J. Biol. Chem. 276:45128-45136(2001).
CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
CC dependent binding to cells. Preferentially binds to alpha2,3-
CC linked sialic acid. The sialic acid recognition site may be masked
CC by cis interactions with sialic acids on the same cell surface.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Predominantly expressed by immature
CC monocytic/myeloid lineage cells in bone marrow. Also found at
CC lower levels in mature neutrophils and monocytes.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
CC as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
CC motif is involved in modulation of cellular responses. The
CC phosphorylated ITIM motif can bind the SH2 domain of several SH2-
CC containing phosphatases.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC (sialic acid binding Ig-like lectin) family C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF293371; AAL11043.1; -.
CC HSSP; Q9Y286; 107S.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC Pfam; PF00047; Ig; 2.
CC -----
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SMART; SMC0408; IGC2; 1.
 PROSITE; PS00835; IG_LIKES; 2.
 Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat;
 SIGNAL; Transmembrane.
 FT SIGNAL 1 16 Potential.
 FT CHAIN 17 569 Stalk acid binding Ig-like lectin-F.
 FT DOMAIN 17 439 Extracellular (Potential).
 FT TRANSMEM 440 460 Potential.
 FT DOMAIN 461 569 Cytoplasmic (Potential).
 FT DOMAIN 18 116 Ig-like V-type.
 FT DOMAIN 139 224 Ig-like C2-type 1.
 FT DOMAIN 229 324 Ig-like C2-type 2.
 FT SITE 536 541 ITIM motif.
 FT SITE 559 564 SLAM-LIKE MOTIF.
 FT DISULFID 35 163 By similarity.
 FT DISULFID 40 96 By similarity.
 FT DISULFID 157 206 By similarity.
 FT DISULFID 265 308 By similarity.
 FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 200 200 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 203 203 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 372 372 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 387 387 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 569 AA; 61476 MW; 8093838090484FC1 CRC64;

Query Match 24.8%; Score 837; DB 1; Length 569;
 Best Local Similarity 35.7%; Pred. No. 1.3e-44;
 Matches 239; Conservative 80; Mismatches 207; Indels 144; Gaps 26;

QY 2 LPLLSLSSLGSOAMDGRFWIRVOSSVMVPEGLCISVPCSPSYPRODWTGSTPAYGYWF 61
 DB 6 LPLLMA---GCLATDG-YSLSVTGSVTQEGLCVFACQVYP---NSKGPVFGYWF 56
 QY 62 KAVTEITTKAPVATNHQSRREVENSTRGRPOLTGDPKAGNCSLVIRDAQMDSEQYFPRVE 121
 DB 57 REGANIFSGSVATNDPQRSVLKEAGRFYLMKGNHNSCLDIRDAQKIDTGTTFYFRD 116
 QY 122 RGSVRYNFMNDGFFLVKVTLSFTPRPDHNTDLTCHVDPSRKGVSAQRTVLRVAYAPR 181
 DB 117 -GS-VKYSFQKS--MLSVLVIALTEVP---NIQVT----- 144
 QY 182 DIVISIRDNTPALEPQPGNVPILEAQKQFRLILC-----AADSQPPATLSWV----- 231
 DB 145 STLV-----GNSTKLCSVPWACEQGTPIFSMMSALTS 180
 QY 232 LQNR-VLSSSHHPGPRPLGLELPGVKAGDSG-RYTCRAENRLG---SQORALDLSVQYPP 286
 DB 181 LGHRTTLLSELNLTPEP-----QDNGTNLTQV-NLPGTGVTVERTQQLSVIYAP 229
 QY 287 ENLRVMVSQANRTVLENLNGTSLPVLQGSCLVCTVTHSSPPARLSWTQRGVLSPSQP 346
 DB 230 QKMTIRVSGDDTGTVKVLSQASLQIQEGESLVCMDNSNPVAVLSWERPTQ--KPFQL 287
 QY 347 SDPGVLELRVQVEHEGETCHARPLGCHVSLSVHSPKLLGPCSWEAEGHLCSC 406
 DB 288 STPAELQLPRALEDQKVIQCAQNSQGAQTASVLSIRSLQLLQGPSCFEGQLHCSC 347
 QY 517 PKRRTQETPRFRSHRSHTILDYINNVPTAGLQKRNQKATPNPRTPLPGAPSPESK 576
 DB 466 RKSSA-----LKVATKGNHLAK-NPASTINS-----ASITS 496
 QY 577 KKKQKQYQLPS--PPEPKSGTQ-----APESQSQBELHYATLNFVGVPRRBRMPK 627
 DB 117 -GS-VKYSFQKS--MLSVLVIALTEVP---NIQVT----- 144
 QY 182 DIVISIRDNTPALEPQPGNVPILEAQKQFRLILC-----AADSQPPATLSWV----- 231
 DB 145 STLV-----GNSTKLCSVPWACEQGTPIFSMMSALTS 180
 QY 232 LQNR-VLSSSHHPGPRPLGLELPGVKAGDSG-RYTCRAENRLG---SQORALDLSVQYPP 286
 DB 181 LGHRTTLLSELNLTPEP-----QDNGTNLTQV-NLPGTGVTVERTQQLSVIYAP 229
 QY 287 ENLRVMVSQANRTVLENLNGTSLPVLQGSCLVCTVTHSSPPARLSWTQRGVLSPSQP 346
 DB 230 QKMTIRVSGDDTGTVKVLSQASLQIQEGESLVCMDNSNPVAVLSWERPTQ--KPFQL 287
 QY 347 SDPGVLELRVQVEHEGETCHARPLGCHVSLSVHSPKLLGPCSWEAEGHLCSC 406
 DB 288 STPAELQLPRALEDQKVIQCAQNSQGAQTASVLSIRSLQLLQGPSCFEGQLHCSC 347
 QY 517 PKRRTQETPRFRSHRSHTILDYINNVPTAGLQKRNQKATPNPRTPLPGAPSPESK 576
 DB 466 RKSSA-----LKVATKGNHLAK-NPASTINS-----ASITS 496
 QY 577 KKKQKQYQLPS--PPEPKSGTQ-----APESQSQBELHYATLNFVGVPRRBRMPK 627

DB 497 SNIALGYFIQHLNEPGSQTKSQPPPLATYPTQKQDEPHELHAYSLSPQGPMP-PKQNTS 555
 QY 628 GTQADYAEVK 637
 DB 556 AMKSVYTEIK 565
 RESULT 11
 Q80ZE2 PRELIMINARY; PRT; 523 AA.
 AC Q80ZE2;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Siglec-F variant.
 GN Name=Siglecs;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=22921108; PubMed=14559209;
 RA Aizawa H., Zimmermann N., Carrigan P.E., Lee J.J., Rothenberg M.E.,
 RA Bochner B.S.;
 RT "Molecular analysis of human Siglec-8 orthologs relevant to mouse
 RT eosinophils: identification of mouse orthologs of Siglec-5 (msiglec-F)
 RT and Siglec-10 (msiglec-G).";
 RL Genomics 82:521-530(2003).
 DR EMBL; AY210401; AAC48274.1; -.
 DR HSSP; Q9Y286; I07S.
 DR MGI; 2681107; Siglecs.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SMC0408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 SQ SEQUENCE 523 AA; 56326 MW; 85342501E33B17EE CRC64;

Query Match 22.9%; Score 772.5; DB 2; Length 523;
 Best Local Similarity 38.5%; Pred. No. 1.4e-40;
 Matches 208; Conservative 63; Mismatches 166; Indels 105; Gaps 20;

QY 2 LPLLSLSSLGSOAMDGRFWIRVOSSVMVPEGLCISVPCSPSYPRODWTGSTPAYGYWF 61
 DB 6 LPLLMA---GCLATDG-YSLSVTGSVTQEGLCVFACQVYP---NSKGPVFGYWF 56
 QY 62 KAVTEITTKAPVATNHQSRREVENSTRGRPOLTGDPKAGNCSLVIRDAQMDSEQYFPRVE 121
 DB 57 REGANIFSGSVATNDPQRSVLKEAGRFYLMKGNHNSCLDIRDAQKIDTGTTFYFRD 116
 QY 122 RGSVRYNFMNDGFFLVKVTLSFTPRPDHNTDLTCHVDPSRKGVSAQRTVLRVAYAPR 181
 DB 117 -GS-VKYSFQKS--MLSVLVIALTEVP---NIQVT----- 144
 QY 182 DIVISIRDNTPALEPQPGNVPILEAQKQFRLILC-----AADSQPPATLSWV----- 231
 DB 145 STLV-----GNSTKLCSVPWACEQGTPIFSMMSALTS 180
 QY 232 LQNR-VLSSSHHPGPRPLGLELPGVKAGDSG-RYTCRAENRLG---SQORALDLSVQYPP 286
 DB 181 LGHRTTLLSELNLTPEP-----QDNGTNLTQV-NLPGTGVTVERTQQLSVIYAP 229
 QY 287 ENLRVMVSQANRTVLENLNGTSLPVLQGSCLVCTVTHSSPPARLSWTQRGVLSPSQP 346
 DB 230 QKMTIRVSGDDTGTVKVLSQASLQIQEGESLVCMDNSNPVAVLSWERPTQ--KPFQL 287
 QY 347 SDPGVLELRVQVEHEGETCHARPLGCHVSLSVHSPKLLGPCSWEAEGHLCSC 406
 DB 288 STPAELQLPRALEDQKVIQCAQNSQGAQTASVLSIRSLQLLQGPSCFEGQLHCSC 347
 QY 407 SSOASPAFLRWLWGLBELLEGNSSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCEAW 466

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Db 348 SRANPAPSLRWLRGEGVLEGNSTVTKSSAGQWANSLLLSMFPSNHRUSCBW 407
QY 467 NVHGAQSSIIQLPKKGLISTAFEN-----GAFIGIGITALLFLICLALII--MKIL 516
Db 408 SDNRVQRATILLVSGPK--VQAGKSETSRGTGLGAIWAGLWALLAVCLCLIFFTKVL 465
QY 517 PKR 519
Db 466 RKX 468

RESULT 12
SILH HUMAN
ID SILH HUMAN STANDARD; PRT; 499 AA.
AC Q9NYZ4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sialic acid binding Ig-like lectin 8 precursor (Siglec-8)
DE (Sialoadhesin family member-2) (SAF-2).
GN Name=SIGLEC8; Synonyms=SAF2;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20549027; PubMed=11095983; DOI=10.1006/bbrc.2000.3866;
RA Fousias G., Yousef G.M., Diamandis E.P.;
RT "Molecular characterization of a siglec8 variant containing
RT cytoplasmic tyrosine-based motifs, and mapping of the siglec8 gene.";
RL Biochem. Biophys. Res. Commun. 278:775-781(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=20314554; PubMed=10856141;
RA Kikly K.K., Bochner E.S., Freeman S.D., Tan K.B., Gallagher K.T.,
RA D'Alessio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller C.L.,
RA Murdoch P.R., Tachimoto H., Schleimer R.P., White J.R.;
RT "Identification of SAF-2, a novel siglec expressed on eosinophils,
RT mast cells, and basophils.";
RL J. Allergy Clin. Immunol. 105:1093-1100(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX TISSUE=Eosinophil;
RX MEDLINE=20092847; PubMed=10625619;
RA Floyd H., Ni J., Cornish A.L., Zeng Z., Liu D., Carter K.C., Steel J.,
RA Crocker P.R.;
RT "Siglec-8, A novel eosinophil-specific member of the immunoglobulin
RT superfamily.";
RL J. Biol. Chem. 275:861-866(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Floyd H., Zhang J.Q., Crocker P.R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
CC dependent binding to cells. Preferentially binds to alpha2,3-
CC linked sialic acid. Also binds to alpha2,6-linked sialic acid. The
CC sialic acid recognition site may be masked by cis interactions
CC with sialic acids on the same cell surface.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Long;
CC IsoId=Q9NYZ4-1; Sequences=Displayed;
CC Name=2;
CC IsoId=Q9NYZ4-2; Sequence=VSP_002559;
CC Name=3;
CC IsoId=Q9NYZ4-3; Sequence=VSP_002560;
CC -!- TISSUE SPECIFICITY: Expressed specifically on eosinophils.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
CC as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
CC motif is involved in modulation of cellular responses. The

```

```

CC phosphorylated ITIM motif can bind the SH2 domain of several SH2-
CC containing phosphatases.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC (sialic acid binding Ig-like lectin) family.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC -----
CC EMBL; AF287892; AAC00573.1; -
CC EMBL; AF223403; AAF34702.1; -
CC EMBL; AF195092; AAF27622.1; -
CC EMBL; AF310234; AAK55140.1; -
CC HSP; Q9Y286; 107S.
CC Genew; HGNC:10877; SIGLEC8.
CC MIM; 605639; -; C:integral to membrane; TAS.
CC GO; GO:0016021; C:integral to membrane; TAS.
CC GO; GO:0005229; F:sugar binding; TAS.
CC GO; GO:0004888; F:transmembrane receptor activity; TAS.
CC GO; GO:0007165; F:signal transduction; TAS.
CC InterPro; IPR003598; Ig_C2.
CC Pfam; PF00047; Ig_2.
CC SMART; SMC0408; IGC2; 1.
CC PROSITE; PS00835; IG_LIKE; 2.
CC Alternative splicing; Cell adhesion; Glycoprotein;
CC Immunoglobulin domain; Lectin; Repeat; Signal; Transmembrane.
FT SIGNAL 1 16
FT CHAIN 17 499
FT DOMAIN 17 363
FT TRANSMEM 364 384
FT DOMAIN 385 499
FT DOMAIN 40 123
FT DOMAIN 157 240
FT DOMAIN 246 344
FT SITE 445 450
FT SITE 468 473
FT DISULFID 42 181
FT DISULFID 47 107
FT DISULFID 175 224
FT DISULFID 283 328
FT CARBOHYD 172 172
FT CARBOHYD 249 249
FT CARBOHYD 267 267
FT VARSPLIC 152 245
FT VARSPLIC 416 499
SQ SEQUENCE 499 AA; 54042 MW; 086BFF989B74123C CRC64;
Query Match 21.4%; Score 721.5; DB 1; Length 499;
Best Local Similarity 30.8%; Pred. No. 2,le-37;
Matches 207; Conservative 80; Mismatches 152; Indels 233; Gaps 21;
Qy 1 MLLPLLSSLLGGSQAVDG-----RFWIRVQSVNVVPEGLCLSVPCSFYPRQDWTGST 54
Db 1 MLLLLILLPLLLWGTGKMGDEGRQYCDGYLLQVQLVTVQEGLCVHVPCSFYPRQDWTGSD 60
Qy 55 PAYGYWFKAVTEITKGAIPVATNHQSREVENSTGRFQLTGDPKAGNCSLVIRDAQMDES 114
Db 61 PVFGVFRAGDRPYQDAPVATNPDPVQAEIQTGRFQLLGDIWNSDCLSLIRAKRKDG 120
Qy 115 QYFFRVERGSYRNFNMNDGFF----LKVTLSFTPRP-----QDHTDLTCHVDV 161

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Q96PQ1; Q8IYH7;
 28-FEB-2003 (Rel. 41, Created)
 28-FEB-2003 (Rel. 41, Last sequence update)
 01-OCT-2004 (Rel. 45, Last annotation update)
 Sialic acid binding Ig-like lectin-like 1 precursor (Siglec-like molecule 1) (Siglec-L1) (UNQ9215/PRO34042).
 Name=SIGLECL1; Synonyms=SLG;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 [1]_TaxID=9606;
 SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 CC TISSUE=Bone marrow;
 CC MEDLINE=21523976; PubMed=11546777; DOI=10.1074/jbc.M105926200;
 CC Angata T., Varki N.M., Varki A.;
 CC Fousias G., Taylor S.M., Yousef G.M., Tropak M.B., Ordon M.H.,
 CC Diamandis E.P.;
 CC "Cloning and molecular characterization of two splice variants of a
 CC new putative member of the Siglec-3-like subgroup of Siglecs.";
 CC J. Biol. Chem. 276:40282-40287(2001).
 CC [2]
 CC SEQUENCE FROM N.A. (ISOFORM LONG).
 CC MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 CC Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 CC Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 CC Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 CC Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 CC Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 CC Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 CC Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yansura D.,
 CC Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 CC Godowski P., Gray A.;
 CC "The secreted protein discovery initiative (SPDI), a large-scale
 CC effort to identify novel human secreted and transmembrane proteins: a
 CC bioinformatics assessment.";
 CC Genome Res. 13:2265-2270(2003).
 CC [4]
 CC SEQUENCE FROM N.A. (ISOFORM LONG).
 CC TISSUE=Blood;
 CC MEDLINE=22382957; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 CC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 CC Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 CC Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 CC Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 CC Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,
 CC Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 CC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 CC Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallus D.E.,
 CC Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.;
 CC "Generation and initial analysis of more than 15,000 full-length human
 CC and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
 CC dependent binding to cells. The sialic acid recognition site may
 CC be masked by cis interactions with sialic acids on the same cell
 CC surface.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

Name=Long; Synonyms=SLG-L;
 IsoId=Q96PQ1-1; Sequence=Displayed;
 Name=Short; Synonyms=SLG-S;
 IsoId=Q96PQ1-2; Sequence=VSP_002566;
 -!- TISSUE SPECIFICITY: The short isoform is highly expressed in
 CC spleen, small intestine and adrenal gland; it is lower expressed
 CC in thyroid, placenta, brain, stomach, bone marrow, spinal chord and
 CC testis. The long isoform is highly expressed in spleen, small
 CC intestine and bone marrow; it is lower expressed in thyroid,
 CC placenta, thymus, trachea, stomach, lung, adrenal gland, fetal
 CC brain and testis.
 CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
 CC as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
 CC motif is involved in modulation of cellular responses. The
 CC phosphorylated ITIM motif can bind the SH2 domain of several SH2-
 CC containing phosphatases.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
 CC (sialic acid binding Ig-like lectin) family C2-type domains.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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 CC -----
 CC EMBL; AF277806; AA51233.1; -;
 CC EMBL; AF277806; AA51234.1; -;
 CC EMBL; AF282256; AA71521.1; -;
 CC EMBL; AY358140; AAQ88507.1; -;
 CC EMBL; BC035809; AAH35809.2; -;
 CC HSP; Q9Y286; I07S.
 CC Genew; HGNC:15482; SIGLECL1.
 CC MIM; 606094; -;
 CC InterPro; IPR007110; Ig-like.
 CC Pfam; PF00047; Ig; 4.
 CC PROSITE; PS00835; IG_LIKE; 3.
 CC Alternative splicing; Cell adhesion; Glycoprotein;
 CC Immunoglobulin domain; Lectin; Polymorphism; Repeat; Signal;
 CC Transmembrane.
 CC SIGNAL 1 18 Potential.
 CC CHAIN 19 595 Sialic acid binding Ig-like lectin-like
 CC -----
 CC DOMAIN 19 481 Extracellular (Potential).
 CC TRANSMEM 482 502 Potential.
 CC DOMAIN 503 595 Cytoplasmic (Potential).
 CC DOMAIN 19 142 Ig-like V-type 1.
 CC DOMAIN 143 269 Ig-like V-type 2.
 CC DOMAIN 275 358 Ig-like C2-type 1.
 CC DOMAIN 365 462 Ig-like C2-type 2.
 CC SITE 563 568 ITIM motif.
 CC SITE 586 591 SLAM-LIKE MOTIF.
 CC By similarity.
 CC By similarity.
 CC By similarity.
 CC By similarity.
 CC By similarity.
 CC N-linked (GlcNAc...) (Potential).
 CC N-linked (GlcNAc...) (Potential).
 CC N-linked (GlcNAc...) (Potential).
 CC N-linked (GlcNAc...) (Potential).
 CC N-linked (GlcNAc...) (Potential).
 CC N-linked (GlcNAc...) (Potential).
 CC N-linked (GlcNAc...) (Potential).
 CC LLLLLPLLCGRVGAKEQKDYLLTMQKSVTVQEGLCVSLC
 CC SFSYPQNGTASDVHGYWFRAGDHVSRNPVANNPARAV
 CC QEETDRFLLGPKDKDCTLSIRDTRSDAGTYVFCVBERG
 CC NMENKYDQLSVNV -> PLLWANEERDSGGWADPRFS
 CC (in isoform Short).
 CC /Ftd=VSP_002566.


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VARIANT      81      81      P -> T (in dbSNP:2034891).
CONFLICT     528     528      R -> W (in Ref. 3).
SEQUENCE     595 AA; 64984 MW; D05662176274C5C3 CRC64;

Query Match      20.7%; Score 700.5; DB 1; Length 595;
Best Local Similarity 31.5%; Pred. No. 5.7e-36;
Matches 196; Conservative 72; Mismatches 176; Indels 179; Gaps 15;

QY 7 LSSLLGSGQAMDRFWIRVQESVWVPEGLICISVPCSFSPRODWTGCTPAYGYWFKAVTE 66
Db 137 LSNVVTASQDLLSRYLEVPESTVQEGLCVSPVCSLVPHYNWTASSEVYGSWFKEGAD 196
QY 67 TTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRVERGSYV 126
Db 197 IPWDIEVATNTPSGKVQEDTHGRFLLGDPQTNCSLSIRDARKGDSKGYFQVERGSR- 255
QY 127 RYFMNDGFLKVTLSFTRP-----PQDHTDLTCHVDFSRKGVGAQRTVRLRVAA 179
Db 256 KMYIYDKLSVHTALHTMPTSPDGLTSGHPRLNLTCSVPWACQGTPTTWMGASVS 315
QY 180 PRDLVISIRDNTPALEPQGNVPYLEAKGQFLRLCAADSPATLSWVLQNRVLSS 239
Db 316 SLD--PTITRSSMLSLIPQDHGTSLTQC----- 343
QY 240 SHPWGPRPLGLELPGVKAGDSGEYTCRAENRLGSOQRALDLSVQYEPENLRVWVSOANRT 299
Db 344 -----VTLPGAGV-----TMTAVRLNISPPQNLNTVFGDGT 378
QY 300 VLENLNGTSLPVLGQSLVLCVTHSSPPARLSWTQRCQVLSQSPQDPDGVLELPRVQV 359
Db 379 ASITLNGSALSVLGQSLHLCAVDSPNPARLSWTGWSLTLSPSQSSNLGLVLELPRVHV 438
QY 360 EHEGETCHARPLGSHQVLSLSV--HYSKPLGPSWEAEGLHCSCSOASAPSLR 417
Db 439 KQEGFTCAQNPGLGSHLSLSLQNEYTGK-----RPI----- 474
QY 418 WVLGEBELGNSQDSFEVTPSSAGFWANSSLSLHGLSSGLRLCEAWNVHGAQSGSIL 477
Db 475 -----SGVTL----- 479
QY 478 QLPDKKGLISTAFNGAFIGITALLFLCLALIMKLPKRQTQTERPRFSRHSITL 537
Db 480 -----GAFGAGATALVFLYFCIIFVW---RSCRKKSARPAVGVGDTCM 521
QY 538 DYINNV---PTAGPLAQKNQKATNSPETPLPP--GAPSPESKKNQKQYOLPSFPEPK 592
Db 522 EDANVRGASQGLI-----ESPADSPPHHAPPALATPSPE-----EGEIYASLSFHK 572
QY 593 SSTQAPESQESQELHYATINFP 615
Db 573 ARQPYQEQEA-IGVYESSINIP 594

RESULT 15
STILL PANTR
ID STILL PANTR STANDARD; PRT; 597 AA.
AC Q95LH0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sialic acid binding Ig-like lectin-like 1 precursor (Siglec-like
DE molecule 1) (Siglec-1).
DE Name=SIGLECL1;
GN Pan troglodytes (Chimpanzee).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777; DOI=10.1074/jbc.M105926200;
RA Argata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
```

```

J. Biol. Chem. 276:40282-40287(2001).
-!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
dependent binding to cells. The sialic acid recognition site may
be masked by cis interactions with sialic acids on the same cell
surface.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
motif is involved in modulation of cellular responses. The
phosphorylated ITIM motif can bind the SH2 domain of several SH2-
containing phosphatases.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
(sialic acid binding Ig-like lectin) family.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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EMBL; AF293372; AAL09302.1; -.
HSSP; Q9Y286; 107S.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; Ig; 4.
SMART; SM00408; IGc2; 1.
PROSITE; PS00835; IG_LIKE; 3.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat;
Signal; Transmembrane.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 597 Sialic acid binding Ig-like lectin-like
FT DOMAIN 21 483 Extracellular (Potential).
FT TRANSMEM 484 504 Potential.
FT DOMAIN 505 597 Cytoplasmic (Potential).
FT DOMAIN 51 144 Ig-like V-type 1.
FT DOMAIN 145 271 Ig-like V-type 2.
FT DOMAIN 277 360 Ig-like C2-type 1.
FT DOMAIN 367 464 Ig-like C2-type 2.
FT SITE 565 570 ITIM motif.
FT SITE 588 593 SLAM-LIKE MOTIF.
FT DISULFID 46 106 By similarity.
FT DISULFID 168 301 By similarity.
FT DISULFID 173 233 By similarity.
FT DISULFID 295 344 By similarity.
FT DISULFID 403 448 By similarity.
FT CARBOHYD 142 142 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 181 181 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 232 232 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 292 292 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 362 362 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 369 369 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 387 387 N-linked (GLCNAC...) (Potential).
SQ SEQUENCE 597 AA; 65075 MW; 74C13CFA93CDB5BA5 CRC64;

Query Match      20.5%; Score 692.5; DB 1; Length 597;
Best Local Similarity 30.7%; Pred. No. 1.8e-35;
Matches 198; Conservative 75; Mismatches 166; Indels 207; Gaps 17;

QY 7 LSSLLGSGQAMDRFWIRVQESVWVPEGLICISVPCSFSPRODWTGCTPAYGYWFKAVTE 66
Db 139 LSNVVTASQDLLSRYLEVPESTVQEGLCVSPVCSLVPHYNWTASSEVYGSWFKEGAD 198
QY 67 TTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRVERGSYV 126
Db 199 IPCDIPVATNTPSGKVQEDTHGRFLLGDPQTNCSLSIRDARKGDSKGYFQVERGSR- 257
QY 127 RYFMNDGFLKVTLSFTRP-----PQDHTDLTCHVDFSRKGVGAQRTVRLRVAY 178
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:18 ; Search time 21.6516 Seconds
(without alignments)
1957.231 Million cell updates/sec

Title: US-09-937-636-4

Perfect score: 3377
Sequence: 1 MLLPILLSLLGSGQMDGR.....RPEARMPKGTQADYAEVKFQ 639

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/protdata/1/aaa/5A_COMB.pep: *
2: /cgn2_6/protdata/1/aaa/5B_COMB.pep: *
3: /cgn2_6/protdata/1/aaa/6A_COMB.pep: *
4: /cgn2_6/protdata/1/aaa/6B_COMB.pep: *
5: /cgn2_6/protdata/1/aaa/PCTUS_COMB.pep: *
6: /cgn2_6/protdata/1/aaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1033	30.6	551	4	US-08-896-537A-2
2	774.5	22.9	421	3	US-08-759-628-5
3	667.5	19.8	431	3	US-09-038-832-2
4	667.5	19.8	431	3	US-09-038-832-2
5	626	18.5	467	3	US-09-046-736-2
6	586.5	17.4	440	3	US-08-759-628-4
7	532.5	15.8	374	3	US-09-046-736-4
8	448.5	13.3	364	4	US-08-896-537A-3
9	237.5	7.0	318	6	5242798-5
10	230.5	6.8	501	2	US-08-408-095-31
11	229	6.8	917	1	US-08-245-295-2
12	229	6.8	917	1	US-08-481-130-2
13	229	6.8	917	1	US-08-656-984A-2
14	229	6.8	917	1	US-08-485-604-2
15	229	6.8	917	2	US-08-487-595-2
16	228.5	6.8	924	1	US-08-481-130-28
17	228.5	6.8	924	1	US-08-656-984A-28
18	228.5	6.8	924	1	US-08-485-604-28
19	228.5	6.8	924	2	US-08-487-595-28
20	225	6.7	1241	3	US-09-040-774-2
21	217.5	6.4	1070	4	US-09-961-403-3
22	214	6.3	607	2	US-08-752-307B-12
23	214	6.3	607	3	US-09-707-802-12
24	214	6.3	607	3	US-09-991-326-12
25	206	6.1	464	2	US-08-602-725-32
26	200.5	5.9	642	1	US-08-217-299-1
27	200.5	5.9	698	2	US-08-602-725-36

28	200.5	5.9	734	2	US-08-389-459A-17	Sequence 17, Appl
29	200.5	5.9	734	3	US-08-987-867A-17	Sequence 17, Appl
30	200	5.9	56	4	US-09-513-999C-4599	Sequence 4599, Ap
31	199.5	5.9	1953	4	US-09-917-254-92	Sequence 92, Appl
32	197.5	5.8	280	4	US-09-270-767-43068	Sequence 43068, A
33	194	5.7	828	1	US-08-261-304-2	Sequence 2, Appl
34	193.5	5.7	1209	4	US-09-130-158A-2	Sequence 2, Appl
35	192.5	5.7	424	6	PCT-US95-08493-13	Patent No. 5169835
36	191.5	5.7	946	5	PCT-US95-08493-13	Sequence 13, Appl
37	191	5.7	529	3	US-09-383-586-31	Sequence 31, Appl
38	191	5.7	529	4	US-09-823-038A-31	Sequence 31, Appl
39	188.5	5.6	630	2	US-08-752-307B-14	Sequence 14, Appl
40	188.5	5.6	630	3	US-09-707-802-14	Sequence 14, Appl
41	188.5	5.6	630	3	US-09-991-326-14	Sequence 14, Appl
42	188	5.6	1091	3	US-08-986-485-5	Sequence 5, Appl
43	187.5	5.6	612	2	US-08-752-307B-11	Sequence 11, Appl
44	187.5	5.6	612	3	US-09-707-802-11	Sequence 11, Appl
45	187.5	5.6	612	3	US-09-991-326-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-896-537A-2
; Sequence 2, Application US/08896537A
; Patent No. 6590088
; GENERAL INFORMATION:
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CD33-Like Protein
; FILE REFERENCE: 1488.0480C01
; CURRENT APPLICATION NUMBER: US/08/896,537A
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 60/022,481
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-896-537A-2

Query March		30.6%	Score 1033;	DB 4;	Length 551;
Best Local Similarity		39.0%	Pred. No. 4.7e-80;		
Matches 253;		Conservative 78;	Mismatches 204;	Indels 114;	Gaps 15;
Qy	2	LLPILLSLL-GGSOAMDGRFWIRVQBSVMVPEGLICISVFCSPYPRQDWTGSTPAYGYW	60		
Db	1	MLPILLSLL-GGSOAMDGRFWIRVQBSVMVPEGLICISVFCSPYPRQDWTGSTPAYGYW	60		
Qy	61	FKAVTETTKGAPVATNHQSRREVMSTGRFOLGDPKAGNCSLVIRDAQODSCYFFRV	120		
Db	61	FRDGEIPYAEVATNPNDRVRKPTQCRFRLLGDVQKNCSLSIGDARMEDTGSYFFRV	120		
Qy	121	ERGSYVYNNMDGFFLKVTLSFTTPQDHTDLTCHVDFSRKGVSAQRTVLRVAYAP	180		
Db	121	ERGRDVKISYQQNKINLEVTAL	142		
Qy	181	RDVLVISRDNTPALEPQPGQNVFYLEAQKQFLRLC----	AADSQPPATLSWLVQNRV	236	
Db	143	-----LESGRPTLSCSLPGSCGAGPLTFSWT--GNA	184		
Qy	237	LSSHPHGPPLGLGLPGVKGAGSGRYTCRAENRLSQ----	QRALDLSVQPPENLAVMV	293	
Db	185	LSPDPTTTSSELTLPREDHGTNTLCQMK-RQGAQVTTERTVQLNVSPQITIF-	242		
Qy	294	SOANRTVLENLNGTSLFVLEGSCLCVVCTHSSPPARLSWTQRQGVLSQSDPGVLE	353		
Db	243	--RNGIALEILQNTSYLPVLEGGQALRLCCAPENPPAHLNFWFGSPALNATPISNTGILE	300		

354 LPRVQVHEGEFTCHARHPLGSHVSLSVHYSPKILQPSCSWEAEGHLCSSQAQPA 413
301 LRRVRAEAGGFTCAQHPLGFIQLNLVSVSLPQLGPGSCWEAEGHLCRCSPAWPA 360
414 PSLRWLGELEEGNSQDSFEVTPSSAGPWNSSLSLHGLSSGLRLPCEANVHGAQS 473
361 PSUCWLEKPLGNSQDSFKVNSPGPWNSSLSLHGLSSGLRLPCEANVHGAQS 420
474 GSILQLPDKKGLISTAFNSGAFIGITALLFLCLALIMKILPKRRTOTETPRFRSRH 533
421 GSVLLQLGRSNL-GTGVVPAALGAGVWALLCICLIFLIVKARRKQA-AGREPKXDD 478
534 STILDVINVVTPAGPLAQRKNQATNSPRTPL-PRGAPSPESKKNQKQYOLPSEPEPK 592
479 ED-----PINGTITTSGRKKPWPDPDQASPGDAPP----- 511
593 SSTQAPESQESBELHVATLNTFGVPRPEARMKPTQA-----DYAEVK 637
512 -----LEEKELHYASLSFSEMK-----SREPKDQEAPOSTTEYSEIK 548

RESULT 2

US-08-759-628-5
Sequence 5, Application US/08759628
Patent No. 6225446

GENERAL INFORMATION:

APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILING DATE: 03-DEC-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0552Q
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-759-628-5

Query Match

Best Local Similarity 22.9%; Score 774.5; DB 3; Length 421;
Matches 186; Conservative 49; Mismatches 146; Indels 71; Gaps 9;

3 LPLLLSSLL-GGSQAMGDFWIRQESVNVMPGGLGISVPCSPSYPRQDWTSTPAYGYWF 61

Db 1 MELLPLLLGSGLOEKPVYELQVQSVTVQEGLCVLVPCSFYSFVWRSWSSPLYYVWF 60
QY 62 KAVTETTKGAPVATNHOSREVEMSTRGRFOLTGDPKAGKNCSLVIRDAQMODESQYFFRVE 121
Db 61 RDGEIPYVAEVAATNDRVVKPETOGRFELLGQVQKNCSLSIGDARMDTGSYFFRVE 120
QY 122 RGSVTVNFNMDGFLLKVTVLSTFTPRQDNDTLTCHVDFSRKGVSAQRTVRLRVAYAPR 181
Db 121 RGRDVKYSYQONKLNLEVTALIEKP-----DIHLSP----- 152
QY 182 DLVISISRDNTPALEPOQGNVPVLEAKGQFLRLCAADSQ-----PPATLSWVLQNRVL 237
Db 153 -----LESGLWRPTLSLSLPGSCVAGPPLTFTSGN----- 184
QY 238 SSSHPWGPRLG---LELPGVKAGDSGRYTCRAENRLGSO---ORALDLSVQYPPENLRV 291
Db 185 AXSAPMTPRXPAPRELTLTPRPEDHGTNLTCOMK-RQGAQVTTXTVQLNVSYAPQTITI 243
QY 292 MVSQANETVLENLGNGTSLPVLEQSLCLVCTHSSPPARLSWTRQGVLSPSQSDPGV 351
Db 244 F---RNGIALEILQNTSYLPVLEQQLRLCUDAPSPAPHLHSWFOQSPALNATPISNTGI 300
QY 352 LELPRVQVHEGEFTCHARHPLGSHVSLSVHYSPKILQPSCSWEAEGHLCSSQAAS 411
Db 301 LELRRVRAEAGGFTCAQHPLGFIQLNLVSVSLPQLGPGSCWEAEGHLCRCSPRAR 360
QY 412 PPSLRWLEGELEEGNSQDSFEVTPSSAGP 443
Db 361 PPSLRWLEGELEEGNSQDSFEVTPSSAGP 392

RESULT 3
US-09-038-832-2
Sequence 2, Application US/09038832
Patent No. 6146845
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-2
TITLE OF INVENTION: (SAF-2)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINIER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
FILING DATE: 11-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50018
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-038-832-2

Query Match      19.8%; Score 667.5; DB 3; Length 431;
Best Local Similarity 39.2%; Pred. No. 7.9e-49;
Matches 162; Conservative 52; Mismatches 102; Indels 97; Gaps 10;

QY 1 MLLPLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSPRODWTGST 54
DB 1 MLLLLLLLLPWLWGTGKMGSDRQYGDGYLLQVQLVTVQEGLCVHVPCSFSPQDGTSD 60
QY 55 PAYGWFKAVTETTKGAPVATNHQREVMSTGRFQLTGDPKAGNCSLVIRDAQMDES 114
DB 61 PVHGWFYFRAGDRPYQDAFVATNPNPREVQAEQGRFQLLGDIWNSDCSLSDARKKDKG 120
QY 115 QYFFRVERGVSRYRNFMDGPE---LKVTVLSFTPRP-----QDHTDLTCHVDF 161
DB 121 SYFFRLERGS-MKWSYKSQLNYKTQKLSVFVTALTHTRPDILLGLTLESGHSENITCSVPW 179
QY 162 SRK-----GVSQRTVRLRVAYAPRDLVISIRDNTPALEPQPGNVVYLEAQKG 211
DB 180 ACKQGTTPMISWIGASVS-----SPGP---TTARSSVLTLPKPDHGTSLTQ-- 225
QY 212 QFLRLLCADSQPPATLSWVLQNRVLSSSHPPGPRPLGLELPGVKAGDSGRYTCRAENRL 271
DB 226 -----VTLPG--TGVTTTSTVR----- 240
QY 272 GSQORALDLSVQYPENLRVMVQANRTVLENLNGTSLPVLGQSLCLVCTHSSPPAR 331
DB 241 -----LDVSYPPNLTMTVFQGDATASTALNGSSLSVLGQSLALVCVNSNPPAR 292
QY 332 LSWTQRGQVLSQSPSDPGVLELPRVQVEHEGEFTCHARHPLGSOHVLSLSV 384
DB 293 LSWTRGSLTLCPSRSSNFGLLPRVHVHVRDEGEFTCRAQNAQGSQHLSLSL 345

RESULT 4
US-09-038-832-4
; Sequence 4, Application US/09038832
; Patent No. 6146845
; GENERAL INFORMATION:
; APPLICANT: KIKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Sialoadhesin Family Member-2
; TITLE OF INVENTION: (SAF-2)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 11-MAR-1998
; CLASSIFICATION:
; APPLICATION NUMBER: 60/041,886
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701

```

```

; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-038-832-4

Query Match      19.8%; Score 667.5; DB 3; Length 431;
Best Local Similarity 39.2%; Pred. No. 7.9e-49;
Matches 162; Conservative 52; Mismatches 102; Indels 97; Gaps 10;

QY 1 MLLPLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSPRODWTGST 54
DB 1 MLLLLLLLLPWLWGTGKMGSDRQYGDGYLLQVQLVTVQEGLCVHVPCSFSPQDGTSD 60
QY 55 PAYGWFKAVTETTKGAPVATNHQREVMSTGRFQLTGDPKAGNCSLVIRDAQMDES 114
DB 61 PVHGWFYFRAGDRPYQDAFVATNPNPREVQAEQGRFQLLGDIWNSDCSLSDARKKDKG 120
QY 115 QYFFRVERGVSRYRNFMDGPE---LKVTVLSFTPRP-----QDHTDLTCHVDF 161
DB 121 SYFFRLERGS-MKWSYKSQLNYKTQKLSVFVTALTHTRPDILLGLTLESGHSENITCSVPW 179
QY 162 SRK-----GVSQRTVRLRVAYAPRDLVISIRDNTPALEPQPGNVVYLEAQKG 211
DB 180 ACKQGTTPMISWIGASVS-----SPGP---TTARSSVLTLPKPDHGTSLTQ-- 225
QY 212 QFLRLLCADSQPPATLSWVLQNRVLSSSHPPGPRPLGLELPGVKAGDSGRYTCRAENRL 271
DB 226 -----VTLPG--TGVTTTSTVR----- 240
QY 272 GSQORALDLSVQYPENLRVMVQANRTVLENLNGTSLPVLGQSLCLVCTHSSPPAR 331
DB 241 -----LDVSYPPNLTMTVFQGDATASTALNGSSLSVLGQSLALVCVNSNPPAR 292
QY 332 LSWTQRGQVLSQSPSDPGVLELPRVQVEHEGEFTCHARHPLGSOHVLSLSV 384
DB 293 LSWTRGSLTLCPSRSSNFGLLPRVHVHVRDEGEFTCRAQNAQGSQHLSLSL 345

RESULT 5
US-09-046-736-2
; Sequence 2, Application US/09046736
; Patent No. 6090582
; GENERAL INFORMATION:
; APPLICANT: KIKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Sialoadhesin Family Member-3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,736
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,885
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F

```

REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-50019
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-046-736-2

Query Match 18.5%; Score 626; DB 3; Length 467;
 Best Local Similarity 28.5%; Pred. No. 3.3e-45;
 Matches 186; Conservative 79; Mismatches 184; Indels 202; Gaps 15;

Qy 2 LLPLLSSLLGGQAMGR-----FWIRVQSSVMVPEGLCTSVPCSPSYPRQDWTGSTP 55
 Db 1 MLLLLLLPLLMGRVEGQSNRKYSLTQSSVTQEGMCVHVRCSPSYPDSTQSDP 60
 Qy 56 AYGYWFKAVTETTKGAPVATNHOSREVENSTGRFOLTGDPKAGKCSLVIRDAQMDQDSQ 115
 Db 61 VHCYWFPRAGNDISWKAFAVATNPAWAVQETDRFHLGDPQTKNCTLSIRDAQMDAGR 120
 Qy 116 YPRVREGSVRYNFMNDGFFKVTVLSTPQDHT-----DLTCHVDPSRKGVSA 168
 Db 121 YFRMEKGN-KWNYKYDQLSVNVTALTRPNILIPGTLESQFQNLTCVSWACEQGT 179
 Qy 169 QRTVRLRVAVAPDLVTSRNTPALEPQPGNVPLYEAKQGFRLRLCAADSOPTAL 228
 Db 180 PMISWMTGVSPPH--PSTRSVLTLLPQPHGTSITCQ----- 218
 Qy 229 SWVLQNRVLSGSHPMGRPLGLEFGVKAGDSGRYTCRAENRLGQQORALDLSVQYP 288
 Db 219 -----VTLPGAGV-----ITNRTIQLNVSPQN 242
 Qy 289 LRWNQANRTVLNLCNGTSLPVLGQSLCLVCVTHSSPPARLSWTORGQVLSQSD 348
 Db 243 LTVTFQGGTASTALGSSSLVLEGQSLRLVCAVDSNPPARLSWTWRSLSLYPSQSN 302
 Qy 349 PGVLELPYQVEHEGFTCHAHPLGSHVLSLSV--HYSKLLGSPSCSWEAEGHCS 406
 Db 303 PLVLEL-QVHLGDEGFTCEAQNLSGSHVLSLSLQOEYTKM----- 345
 Qy 407 SQGASPAFLRWLWGLGELLEGNSQDSFEVTPSSAGPWANSLSLHGGLSGRLRCEAW 466
 Db 346 ----RPV----- 348
 Qy 467 NVHQAQSGSILQIPDKKGLISTAFNSGAPLIGITALLFLCLALIMKILPKRTQETP 526
 Db 349 -----SGVLL-----GAVGGAGATLVFLSPCVIFIV--RSCRKXSA 384
 Qy 527 RPFERHSTILDYINVVPTAGLAQRNQAATNSPRTPLPGAPSPSKNKKQYQLP 586
 Db 385 RP-----AADVDGVGMK-----DANTIRGSASQGNLTESW 414
 Qy 587 SPFEKSSSTQAPESQESQELHYATLNFPGVPRPEARMKGTQADYAEVK 637
 Db 415 AADNPRHHGLAAHSSGEEREIQYAPLSFKXGEPQ-DLSGQEAATNNEYSEIK 464

RESULT 6

US-08-759-628-4

Sequence 4, Application US/08759628

Patent No. 6225446

GENERAL INFORMATION:

APPLICANT: Altman, Scott W.

APPLICANT: Rock, Fernando L.

APPLICANT: Bazan, J. Fernando

APPLICANT: Kastelein, Robert A.

TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,628
 FILING DATE: 05-DEC-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,574
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0552Q
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 440 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-759-628-4

Query Match 17.4%; Score 586.5; DB 3; Length 440;

Best Local Similarity 24.7%; Pred. No. 7.4e-42;

Matches 172; Conservative 73; Mismatches 133; Indels 317; Gaps 15;

Qy 2 LLPLLSSLLGGQAMGRFWIRVQSSVMVPEGLCTSVPCSP--SYPRQDWTGSTPAYGY 59

Db 1 MLPLLPLLMWAGALQERRPQLGSPESLTVQEGLCVLVPCRLPTTLF-----ASYGYGY 55

Qy 60 WFKAVTETTKGA--PVATNHOSREVENSTGRFOLTGDPKAGKCSLVIRDAQMDQDSQYF 117

Db 56 WF-----LEGADVATNDPDEEVQETGRPFLLWDPKRNKCSLSIRDARRDNAAVF 109

Qy 118 FRVERGSYVRYNFMNDGFFLKV----- 139

Db 110 FRL-KSKWKYGYTSKIVYRVWALTRPMISIPGWPSSNLTCSVPWVCEQGTPIF 168

Qy 140 -----TVLSFTPRQDHTDLTCHVDPSRKGVSAQRTVRLRVAVAPRD 182

Db 169 SWMSAAPHLLGPRITTSVLTITP-AQDHSNTLTCQVTFPGAVTMTERTIQLNVSAPOK 227

Qy 183 LVTSISRDNTPALEPQPGNVPLYEAKQGFRLRLCAADSOPTALSWVLQNRVLSSSH 242

Db 228 VALSIQNSAAPK-----ILQNT----- 246

Qy 243 WGPRLGLELPGVKAGDSGRYTCRAENRLGQQORALDLSVQYPENLRVWVQANVTILE 302

Db 247 ----- 246

Qy 303 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTORGQVLSQSDPGVLELPVQVHEH 362

Db 247 -----SSLPLGQALRLCLLDAGNPPAHLWFCASPFXNATPISNTGVLELPQVSAE 301

Qy 363 GETCHARHPLGSHVLSLSVHYSKLLGSPSCSWEAEGHLCSCSSQASPAFLRWLWGL 422

Db 302 GDFTCAQHPGLSLQISLSLFVH-----WKPEG----- 329

QY 423 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRCEANWVHGAQSGSILQLPDK 482
Db 330 -----RAGGVL----- 335
QY 483 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTOTETPRPRESRSTILDYINV 542
Db 336 -----GAVGASITTLVFLCVCFIF-----RVKTRKKQPSOCKYTDVNP 376
QY 543 VTAGLAQKRNQKATPNSRPTPLPGAPSPESKKNQKQVLPSPFPKPSSTQAPESQE 602
Db 377 VNVSG-----SRGHQHQFQTGIVSDHPAEAGPISE 406
QY 603 SDEELHYATLNPFGVYRPRPEARMKPGTQADYAEVK 637
Db 407 DEQELHYAVLHPHKVQPOE-----PKVTDTEYSEIK 437

RESULT 7

US-09-046-736-4
; Sequence 4, Application US/09046736
; Patent No. 6090582
; GENERAL INFORMATION:
; APPLICANT: KIKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Sialoadhesin Family Member-3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,736
; FILING DATE: 24-Mar-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,885
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-046-736-4

Query Match 15.8%; Score 532.5; DB 3; Length 374;
Best Local Similarity 25.2%; Pred. No. 2.5e-37;
Matches 162; Conservative 64; Mismatches 137; Indels 281; Gaps 12;
QY 2 LPLLLLSLLGSGQANDGR-----FWIRVQBSVMYPEGICISVPCSFSPYRQDWTGSP 55
Db 1 MLLLLLPULLWGRVERVEWOKNRKDYSLTMQSSVTVQEGNCHVRCFSFYPVDSQSDSP 60
QY 56 AYGVFWKAVTETTKGAPVATNHQSRVEMSTRGRFOLTGDPKAGNCSLVIRDAQMDESEQ 115
Db 61 VHGWFWRAGNDISWKAIPVATNFAWVQEBETRDPRHLLGDPQTKNCTLSIRDARMSDAGR 120

QY 116 YFRVVRGSRVYRNFVNDGFFLKVTVLSFTPRPDHNTDLTCHVDPSRKVSAQRTVRLR 175
Db 121 YFRMEKGN-IKNKYKD----- 137
QY 176 VAVAPRDLVISGRDNTPALEPOQGNVPYLEAQKGQFLRLCAADSQPPATILSVLQNR 235
Db 138 ----- 137
QY 236 VLSSHPWGPRLGLELPGVAGDSGRYTCRAENRIGSQORALDLSVQYPPENLRVMVSQ 295
Db 138 -----QLSVNVTYPQNLTVTVFQ 156
QY 296 ANRTVLNLTGNTSLPVLGQSILCVTHSSHSPARLSWTORGQVLSPSPQSDPGVLELP 355
Db 157 GEGTASTALGNSSLSVLGQSRLRLCAVDNPNPARLSWTWRSRLTLYPSPQSNPLVLEL- 215
QY 356 RVQVEHEGETCHARHPLGSHVLSLSV--HYSPLKLLGSCSWAEGLHCLSCSSQASPA 413
Db 216 QVHLGDEGETCRAQNSLGSQHVSLNLSQLQOEVTKM-----RPV 255
QY 414 PSLRWLGBELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRCEANWVHGAQS 473
Db 256 -----S 256
QY 474 GSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTOTETPRPRESR 533
Db 257 GVLL-----GAVGAGATALLVFLSFCVFIW--RSCRKKSARP----- 293
QY 534 STILDYINVVPTAGPLAQKRNQKATPNSRPTPLPGAPSPESKKNQKQVLPSPFPKPS 593
Db 294 -----AADVGDIGMK-----DANTIRGSASQGNLTESWADDNPRH 328
QY 594 STQAPESQESQELHYATLNPFGVYRPRPEARMKPGTQADYAEVK 637
Db 329 HGLAAHSGEREIQYAPLSFHKEPQ-DLSQGEATNNEISEIK 371

RESULT 8

US-08-896-537A-3
; Sequence 3, Application US/08896537A
; Patent No. 6590088
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CD33-Like Protein
; FILE REFERENCE: 1488.0480001
; CURRENT APPLICATION NUMBER: US/08/896,537A
; CURRENT FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 60/022,481
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 3
; LENGTH: 364
; TYPE: PPT
; ORGANISM: Homo sapiens
US-08-896-537A-3

Query Match 13.3%; Score 448.5; DB 4; Length 364;
Best Local Similarity 21.4%; Pred. No. 3.9e-30;
Matches 149; Conservative 48; Mismatches 110; Indels 389; Gaps 11;

QY 1 MLLPLLLLSLGSGQANDGRFWIRVQBSVMYPEGICISVPCSFSPYRQDWTGSPAYGYW 60
Db 1 MPLLLLLPULLWAGALANDPNFWLQVQBSVTVQEGLCVLVPTFFPHPIPYDKNSPVEHYW 60
QY 61 PKAVTEITKGAPVATNHQSRVEMSTRGRFOLTGDPKAGNCSLVIRDAQMDESEQYFRV 120
Db 61 FREGAILSGDSPVATNKLDQVQEBETQGRFKLLGDPGRNNCSLIVDARRDNGSYFRM 120
QY 121 ERGSYVRVNFVNDGFFLKVTV----- 140

121 ERGS-TKYSKSPOLS VHVDTLTHRPKILIPGLTLEPGHSHKNTLCSVSWACEQGTPIPSM 179
141 -----VLSFTPRPDHNTDLTCHVDFSRKGSQAQTVRLVAYAPRDV 184
180 LSAPTSLGPRTHSSVLIITPRPDHNTLCOVKFAGAVTERTIGLVYYP----- 235
185 ISIRDNTPALEPQPNQVPLEAQKQGLRLILCAADSPAPFLSVLQNRVLSSSHWP 244
236 -----QNPT----- 240
245 PRFLGLELPGVACD-SGRYTCAENRLGSGQALDLSVOYPPENLRVMVQANRTVLEN 303
241 -----GIFPDGSGKQETRA----- 255
304 LGNGTSLPVGQSLCLVCVTHSSPPARLSWTQGVLSQSPSDGVLPRVQVEHEG 363
256 ----- 255
364 EFTCHARHPLGSHVLSLSVHVSXKLGLPSCSWEAEGHLCSCSQSPAPSLRWLGE 423
256 ----- 255
424 LLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCEANVHGAGSSILQIPDK 483
256 -----GL-----VHGAIGGA----- 265
484 GLISTAFSGAPLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 543
266 -----GVTALLALCLLFFIVKTHRKAARTAVGNDTHPT----- 302
544 PTASPLAQKXKATNSRTPLPQAPSPEKXKXQYQLSPPEKSSSTQAPESQBS 603
303 -----TGSASPKQKXK-----LHGETTSSCSGAAPTVM 334
604 QEELHYATLNFQVRPRPEARMPKGTQADYAEVKFQ 639
335 DEELHYASLNFHGNP-----SKDTSTSEYSEVRTO 364

RESULT 9

3242798-5

Patent No. 5242798

APPLICANT: SUTCLIFFE, J. GERGO

TITLE OF INVENTION: SYNTHETIC POLYPEPTIDES CORRESPONDING
TO PORTIONS OF PROTEINOLIDS TRANSLATED FROM BRAIN-SPECIFIC MRNAs,

RECEPTORS, METHODS AND DIAGNOSTICS USING THE SAME

NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA:

FILING DATE: 07-FEB-1990

PRIORITY APPLICATION DATA:

FILING DATE: 03-JUN-1987

APPLICATION NUMBER: 516,136

FILING DATE: 21-JUL-1983

SEQ ID NO: 5

LENGTH: 318

5242798-5

Query Match 7.0%; Score 237.5; DB 6; Length 318;
Best Local Similarity 25.1%; Pred. No. 4.2e-12;
Matches 95; Conservative 60; Mismatches 146; Indels 77; Gaps 13;

QY 272 GSOQRALDLSVQYPPENLRVMVQANRTVLENLGHGTSIPVLEGOSLGLVCVTHSSPPAR 331
DB 4 GQDNRTVELSVNYAPKPTV-----NGTVAV-EGEIVLSLSTQSNPDPI 48
QY 332 LSWTQGVLSQSPSDGVLPRVQVEHEGFTCHARHPLGSHVLSLSVHVSXKL 391
DB 49 LTIKFKQILATVIVESQLQLEPAVTPEDDGEYWCVAENQYQQRATAFNLSEVAFIIL 108
QY 392 GPS-CSWEAEGHLCSCSQSPAPSLRWLGLLEGNSSQDSFEVTPSSAGPWANSSLS 450

DB 109 LESHCAARDTVQCLVVKSNPPEVAFELPSRNVTVNETEREP-VYSERSGLLLTILT 167
QY 451 LHGLSSGLRLRCEANVHGAGSSILQIPDKKGLISTAFSNG-----AFLGIGITALLF 505
DB 168 LRGOAQPAPPRVICTSRNLYGTQS---LELP-----FGAHLNMWAKIGPVGAVAF 215
QY 506 LCLALIMKILPKRTQTETPRFRSHSTILDYINVVPTAGPLAQKXKATNSRTP 565
DB 216 ALLTAIVCYITQTRKKNVTESPSFS-----AG-----DNPVL 249
QY 566 LPP-----GAPSP-ESKXKXQYQLSPPEKSSSTQAPESQBSQELHYATLNFQVRP 619
DB 250 YSPFRISGAPDKYSEKRLGSRRLGL-----RGEPELDLSYSHSDL-GKRP 298
QY 620 RPEARMPKGTQADYAEVK 637
DB 299 TKDSYTLTEELAEYAEIR 316

RESULT 10

US-08-408-095-31

Sequence 31, Application US/08408095

Patent No. 5858678

GENERAL INFORMATION:

APPLICANT: Chinnadurai, Govindaswamy

TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGRUE, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/408,095

FILING DATE: 21-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mack, Susan J.

REGISTRATION NUMBER: 30,951

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)293-7060

TELEFAX: (202)293-7860

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 501 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-408-095-31

Query Match 6.8%; Score 230.5; DB 2; Length 501;
Best Local Similarity 20.8%; Pred. No. 3.3e-11;
Matches 138; Conservative 66; Mismatches 219; Indels 239; Gaps 29;

QY 24 RVQESVNVVPEGLICISVPCSPSYPRQDWTGTTPAYGWFKAVTETT-----KGAPVAIN 76
DB 30 RTEKVHPIKIL-----PWHAGT-----YSCVAENILGTGORGGAELDVQ 70
QY 77 HQSREVEMSTRGRFQL-TGDPKNGNSLVIRDAQODESQYFRVERGYSYVNFENMGDF 135
DB 71 YPPKKVTVIQNPMPIREGDVTVLSGN-----YNSNPSVTYEMKPHGA 115
QY 136 F-----LKVTVLSLTPRPQDHTDITCHVDFSRKGSQAQTVRLVAYAPRDVVIS 188
DB 116 WEPEGLVKLIQNVG-----DNTTIAC-----ARCNSWCWSAPVALNVQYAPRDVVRKI 167

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,130
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,295
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32713
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 917 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-481-130-2

Query Match 6.8%; Score 229; DB 1; Length 917;
Best Local Similarity 24.8%; Pred. No. 1.1e-10;
Matches 112; Conservative 49; Mismatches 146; Indels 144; Gaps 22;

QY 32 PEGLCISVPCSFYPRQDWTGTPAYGWFKAVTETTKGAPVATNHQSRVEMSTRGRFQ 91
DB 335 PEGKWTVC-----WAGA-----RALV-TLEGIPAVPGQPAELQIN----- 371
QY 92 LTGDFAKGNCSLVIRDAQMDQESQYFFRVERGSYYRNFMDGFFLKVTVLSFTPRPOH 151
DB 372 -----VTKNDDKRGFF----- 382
QY 152 NTDLTCHVDFS--RKGVSQRTVRIRVAYAPR--DLVVISRDNTPALEPOQGNVPYLE 207
DB 383 -CDAALDDVGETLRNQSE-----LRVYAPRLDLD-----DCPSWTWPEPEQTLH 430
QY 208 AQKGQFLRLCAADSQPATLSLWLNQNRVLSSSHFPGPRPLGLEPFG-VKAGDSRYTCR 266
DB 431 -----CEARGNPEPS-----VHCAREDDGAVLALGLLGPVTRALAGTYRCT 471
QY 267 AENRLGSGQRALDLSVQYPPENLRVWVSQANRTVLNNGTSLPVLQGSCLVCVTHS 326
DB 472 AINGQSQAVKQVTLTVEYAP-----ALDSVGCPEFRTWLEGTSEASLSCVAHG 518
QY 327 SPPARLSWTORGQVLSPSQPSDPGVLELP-RVOVEHEGEFTCHARHPLGSGHQVLSLSVH 385
DB 519 VPPSPVSCVRSCK-----EEWMEGLVAREHAGTYRCEALNAGSAAKNVATVE 569
QY 386 YSPKL--LGPSCSW--EAELHCSQSGAPAPSLRWLWLGSELLEGNSQDSPEVTPSS 440

DB 570 YGFSFEELGCFSNWTWVEGSGKLFSCVEVDKPRVE-CVGS---EGASEGVVLPVSSN 625
QY 441 AGPWANSSLSLHGLSGLRLRCEANNVHGA 471
DB 626 SG--SRNSMT-PGNLSEGYL-CNATNRHGS 652
RESULT 13
US-08-656-984A-2
Sequence 2, Application US/08656984A
Patent No. 5753502
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, C'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/656,984A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,295
FILING DATE: 18-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,604
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/33321
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 917 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-656-984A-2
Query Match 6.8%; Score 229; DB 1; Length 917;
Best Local Similarity 24.8%; Pred. No. 1.1e-10;
Matches 112; Conservative 49; Mismatches 146; Indels 144; Gaps 22;

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QY 32 PEGLCISVPCSFSPYPRQDWTGTPAYGWFKAVTETTKGAPVATNHQSRVEMSTRGRFQ 91
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 335 PEGKMTVSC-----WAGA-----RALV-TLEGIPAAVPGQPAELQLN----- 371
QY 92 LTGDPAKNCSLVIRDAQMDQESQYFFRVERGSYVRYNFMNDGFFLKVTVLSFTPRQDH 151
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 372 -----VTKNDDKRGFF----- 382
QY 152 NTDLTCHVDFS--RKGVSQARTVRLRVAYAPR--DLVISISRDNTPALEPOQGNVPYLE 207
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 383 -CDALDVGGETLRKNQSE-----LRVLYAPRLDDL-----DCPRSMTWPEGPEQTLH 430
QY 208 AQKGQFLRLCAADSQPPATLSWLVQNRLVSSHPWGPRLGLELPG-VKAGDSGRYTCR 266
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 431 -----CEARGNPEPS-----VHCARDGGAVLALGLLGPVTRALAGTYRCT 471
QY 267 AENRLGSOQALDLSVOYPPENLRVMVSOANRVLNENLNGTSLPVLEGQSLCLVCVTHS 326
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 472 AINGGQAVKQVTLIVEAP-----ALDSVGCPEITWLEGTEASLSCVAHG 518
QY 327 SPARLSMTQRGQVLSPQSPDPGVLELP-RVOVEHEGEFTCHARHPLGSHVLSLSVH 385
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 519 VPPPSVSVRSK-----EEVMEGLRVAREHAGTYRCEAINARGSAAKNVAVTVE 569
QY 386 YSPKL--LGPSCSW---EAEGLHCSSQASAPSLRWLWLGELLEGSSQDSFEVTPSS 440
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 570 YGPFSEELGCPNSMTWVEGSGKLFCEVDGKPEPRVE-CVGS---EGASEGVVLPLVSSN 625
QY 441 AGPWANSSLSLHGSLSSGLRLRCEANNVHGA 471
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 626 SG--SRNSMT-PGNLSPGIYL-CNATNRHGS 652
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RESULT 14

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US-08-485-604-2
; Sequence 2, Application US/08485604
; Patent No. 5773293
; GENERAL INFORMATION:
; APPLICANT: WF, W. Michael
; APPLICANT: Kilgannon, Patrick D.
; TITLE OF INVENTION: ICAM-4 Materials and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; City: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,604
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
```

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; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,295
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, JR. JOSEPH A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32715
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 917 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-604-2
; Query Match 6.8%; Score 229; DB 1; Length 917;
; Best Local Similarity 24.8%; Pred. No. 1.1e-10;
; Matches 112; Conservative 49; Mismatches 146; Indels 144; Gaps 22;
QY 32 PEGLCISVPCSFSPYPRQDWTGTPAYGWFKAVTETTKGAPVATNHQSRVEMSTRGRFQ 91
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 335 PEGKMTVSC-----WAGA-----RALV-TLEGIPAAVPGQPAELQLN----- 371
QY 92 LTGDPAKNCSLVIRDAQMDQESQYFFRVERGSYVRYNFMNDGFFLKVTVLSFTPRQDH 151
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 372 -----VTKNDDKRGFF----- 382
QY 152 NTDLTCHVDFS--RKGVSQARTVRLRVAYAPR--DLVISISRDNTPALEPOQGNVPYLE 207
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 383 -CDALDVGGETLRKNQSE-----LRVLYAPRLDDL-----DCPRSMTWPEGPEQTLH 430
QY 208 AQKGQFLRLCAADSQPPATLSWLVQNRLVSSHPWGPRLGLELPG-VKAGDSGRYTCR 266
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 431 -----CEARGNPEPS-----VHCARDGGAVLALGLLGPVTRALAGTYRCT 471
QY 267 AENRLGSOQALDLSVOYPPENLRVMVSOANRVLNENLNGTSLPVLEGQSLCLVCVTHS 326
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 472 AINGGQAVKQVTLIVEAP-----ALDSVGCPEITWLEGTEASLSCVAHG 518
QY 327 SPARLSMTQRGQVLSPQSPDPGVLELP-RVOVEHEGEFTCHARHPLGSHVLSLSVH 385
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 519 VPPPSVSVRSK-----EEVMEGLRVAREHAGTYRCEAINARGSAAKNVAVTVE 569
QY 386 YSPKL--LGPSCSW---EAEGLHCSSQASAPSLRWLWLGELLEGSSQDSFEVTPSS 440
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 570 YGPFSEELGCPNSMTWVEGSGKLFCEVDGKPEPRVE-CVGS---EGASEGVVLPLVSSN 625
QY 441 AGPWANSSLSLHGSLSSGLRLRCEANNVHGA 471
  ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 626 SG--SRNSMT-PGNLSPGIYL-CNATNRHGS 652
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RESULT 15

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US-08-487-595-2
; Sequence 2, Application US/08487595
; Patent No. 5852170
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Kilgannon, Patrick D.
; TITLE OF INVENTION: ICAM-4 Materials and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; City: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
```

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,595
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,689

FILING DATE: 27-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/869,724

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,266

FILING DATE: 22-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/245,295

FILING DATE: 18-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: WILLIAMS, JR. JOSEPH A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32714

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 917 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-487-595-2

Query Match 6.8%; Score 229; DB 2; Length 917;

Best Local Similarity 24.8%; Pred. No. 1.1e-10; Mismatches 146; Indels 144; Gaps 22;

Matches 112; Conservative 49;

QY 32 PEGLCISVPCFSYPRQDWTGTPAYGWFKAVTETTKGAPVATNHQSRVEMSTRGRFQ 91

DB 335 PEGKMVTSC-----WAGA-----RALV-TLEGIPAAVPGQPAELQLN----- 371

QY 92 LTGDPAKGNCSLVIRDAQMDSEQYFFRVERGSYVRYNPMNDGPFLLKVTVLSTFTRPDH 151

DB 372 -----VTXNDKRGFF----- 382

QY 152 NTDLTCHVDFS--RKGVSAQRTVRLRVAYAPR--DLVISISRDNTFALEPQGNVPYLE 207

DB 383 -CDAALDVGTETLRKQSS-----LRVLVAPRLDL-----DCPRSWTWPEGEQTLH 430

QY 208 AOKGQELRLLCADSQPPATLSNVLQNRVLSSHPWGPRLGLELPG-VKAGDSGRYTCR 266

DB 431 -----CEARGNPEPS-----VHCARPQGGAVLALGLLGPVTRALAGTYRCT 471

QY 267 AENRLGSGQALDLSVQYPPENLRVWVSQANRTVLENLNGTSLPVLGGQSLCLVCVTHS 326

DB 472 AINGQCAVKQVTLTVVAP-----ALDSVCCPERITWLEGTASLCVANG 518

QY 327 SPPARLSWTQRGVTLSPQSFDPGVLELP-RVQVEHEGEFTCHAHPLGSOHVSLSLVH 385

DB 519 VPPEPSVSCVRSGK-----EENMEGLRVAREHAGTYRCEAINARGSAAKNVAATVE 569

QY 386 YSPKL--LQPSCSW---EABGLHCSCSQASAPSLRWLGLBELLEGNSSQDSFEVTPSS 440

Db 570 YGPSFEELGCPSNWTWVEGSGKLFSCVEVGKPEPRVE-CVGS---EGASRGVVLPVYSSN 625

QY 441 AGPWANSSLSLHGLSSGLSLRCEANVHGA 471

Db 626 SG--SRNSMT-PGNLSPGIYL-CNATRRHGS 652

Search completed: November 5, 2004, 13:58:25

Job time : 25.6516 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 74.3927 Seconds
(without alignments)
3081.324 Million cell updates/sec

Title: US-09-937-636-4

Perfect score: 3377
Sequence: 1 MLLPILLSLLGGQAMDR.....RPEARMPKGTQADYAEVKFQ 639

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 23Sep04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3377	100.0	639	2 AAW81023	AAW81023 Human sia
2	3377	100.0	639	3 AAY97543	AAY97543 Human obe
3	3354	99.3	639	3 AAB25580	AAB25580 CD33-like
4	3354	99.3	639	6 ADA27052	ADA27052 Human nov
5	3354	99.3	639	8 ADA86582	ADA86582 Novel hum
6	3338	98.8	697	5 AAU87087	AAU87087 Sialic ac
7	3334	98.7	697	6 ADA27153	ADA27153 Human nov
8	3334	98.7	697	7 ADD26582	ADD26582 Siglec-10
9	3334	98.7	697	8 ADI37010	ADI37010 Novel hum
10	3334	98.7	697	8 ADL82805	ADL82805 Human PRO
11	3289	97.7	622	5 AAU87075	AAU87075 Sialic ac
12	3174.5	94.0	710	7 ADL19314	ADL19314 Human sec
13	2803.5	83.0	544	5 AAU87074	AAU87074 Sialic ac
14	2790.5	82.6	544	2 AAY411724	AAY411724 Human PRO
15	2790.5	82.6	544	3 AAB444280	AAB444280 Human PRO
16	2790.5	82.6	544	4 AAU29082	AAU29082 Human PRO
17	2790.5	82.6	544	6 ABU58458	ABU58458 Human PRO
18	2790.5	82.6	544	6 ABU88006	ABU88006 Novel hum
19	2790.5	82.6	544	6 ABU84321	ABU84321 Human sec
20	2790.5	82.6	544	6 ABR66195	ABR66195 Human sec
21	2790.5	82.6	544	6 ABR65585	ABR65585 Human sec
22	2790.5	82.6	544	6 ABU95925	ABU95925 Human sec
23	2790.5	82.6	544	6 ABU82764	ABU82764 Human PRO
24	2790.5	82.6	544	6 ABU89885	ABU89885 Novel hum
25	2790.5	82.6	544	6 ABR68134	ABR68134 Human sec

ALIGNMENTS

RESULT 1

AAW81023
ID AAW81023 standard; protein; 639 AA.

XX AC AAW81023;

XX DT 26-APR-1999 (first entry)

XX DE Human sialoadhesin family 4 (SAF-1) polypeptide.

XX KW SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer; inflammation; autoimmune disease; allergy; asthma; inflammation; cerebellar degeneration; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; head injury; septic shock; sepsis; stroke; osteoporosis; osteoarthritis; ischemia reperfusion injury; cardiovascular disease; kidney disease; liver disease; myocardial infarction; hypotension; hypertension; AIDS; myelodysplastic syndrome; aplastic anaemia; baldness; infection.

XX OS Homo sapiens.

XX PN WO9853840-A1.

XX PD 03-DEC-1998.

XX PF 27-MAY-1998; 98WO-US010791.

XX PR 27-MAY-1997; 97US-0047572P.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Kikly KK, Erickson-Miller CL;

XX DR WPI; 1999-080779/07.

XX DR N-PSDB; RAV99911.

XX PT New sialoadhesin family 4 polypeptides and polynucleotides - useful to treat various diseases associated with SAF-4 expression.

XX PS Claim 1; Page 31; 48pp; English.

XX CC This is the amino acid sequence of new human sialoadhesin family 4 (SAF-4), as deduced from the nucleotide sequence of an isolated cDNA clone (see AAV99911). SAF-4 polynucleotides and polypeptides, and methods for producing such polypeptides in transformed host cells using recombinant techniques are disclosed. SAF-4, its agonists and antagonists, and nucleic acid molecules that enhance or inhibit SAF-4 expression, may be used to treat patients in need of enhancement or inhibition of SAF-4

26 2790.5 82.6 544 6 ABU96187 Novel hum
27 2790.5 82.6 544 6 ABU92618 Human sec
28 2790.5 82.6 544 6 ABO08695 Human sec
29 2790.5 82.6 544 6 ABO02747 Human sec
30 2790.5 82.6 544 6 ABR74901 Human sec
31 2790.5 82.6 544 6 ABR94663 Human sec
32 2790.5 82.6 544 6 ABO25226 Novel hum
33 2790.5 82.6 544 6 ABU85636 Human PRO
34 2790.5 82.6 544 6 ABU98796 Novel hum
35 2790.5 82.6 544 6 ABU98011 Novel hum
36 2790.5 82.6 544 6 ABU91717 Novel hum
37 2790.5 82.6 544 6 ABU72232 Novel hum
38 2790.5 82.6 544 6 ABU98410 Human PRO
39 2790.5 82.6 544 6 ABU86251 Human sec
40 2790.5 82.6 544 6 ABU67464 Human sec
41 2790.5 82.6 544 6 ABU80492 Human PRO
42 2790.5 82.6 544 6 ABR99410 Human sec
43 2790.5 82.6 544 6 ABR98800 Human sec
44 2790.5 82.6 544 6 ABO16323 Human sec
45 2790.5 82.6 544 6 ABR92223 Human sec

expression or activity. Conditions that may benefit from such treatment include cancer, inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury damage and other neurological disorders, septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemia reperfusion injury, cardiovascular disease, kidney disease, liver disease, ischemic injury, myocardial infarction, hypertension, hypertension, AIDS, myelodysplastic syndromes and other haematologic abnormalities, aplastic anaemia, male baldness pattern and bacterial, protozoal, fungal and viral infections related to SAP-4 polypeptide activity. Methods of identifying agonists, antagonists/inhibitors are also provided, as well as diagnostic assays for detecting diseases associated with inappropriate SAP-4 activity or levels

XX Sequence 639 AA;

Query Match 100.0%; Score 3377; DB 2; Length 639;
 Best Local Similarity 100.0%; Pred. No. 2.3e-232;
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLPILLSLLGSGQAMDGFRFIRVQESVNVPEGLCISVPCSFSPRQDWTGTPAYGYW 60
 DB 1 MLLPILLSLLGSGQAMDGFRFIRVQESVNVPEGLCISVPCSFSPRQDWTGTPAYGYW 60
 QY 61 FKAVTTTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFVRV 120
 DB 61 FKAVTTTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFVRV 120
 QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSAQTVRLVAYAP 180
 DB 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSAQTVRLVAYAP 180
 QY 181 RDLVISISRDNTPALPEPQGNVPYILEAQKGQFLRLCAADSQPPATLSWLVQNRVLSS 240
 DB 181 RDLVISISRDNTPALPEPQGNVPYILEAQKGQFLRLCAADSQPPATLSWLVQNRVLSS 240
 QY 241 HPWGPRPLGLELPGVKGAGSGRVTCAENRIGSQORALDLSVQYPPENLRVWVSQANRTV 300
 DB 241 HPWGPRPLGLELPGVKGAGSGRVTCAENRIGSQORALDLSVQYPPENLRVWVSQANRTV 300
 QY 301 LENLNGTSLPVLGGQSLCIVCVTHSSPPARLSWTRQGVLSQPSQSDPGVLELPRVQVE 360
 DB 301 LENLNGTSLPVLGGQSLCIVCVTHSSPPARLSWTRQGVLSQPSQSDPGVLELPRVQVE 360
 QY 361 HEGEFTCHARHPLGSHVSLSVHYSPKILGPSCSWEAEGHLCSSQASAPSLRWL 420
 DB 361 HEGEFTCHARHPLGSHVSLSVHYSPKILGPSCSWEAEGHLCSSQASAPSLRWL 420
 QY 421 GELLGNSQDSFEVTPSSAGFWANSLSLHGLSSGLRLRCEANNVHGAQSGSILQLP 480
 DB 421 GELLGNSQDSFEVTPSSAGFWANSLSLHGLSSGLRLRCEANNVHGAQSGSILQLP 480
 QY 481 DKKGLISTAFNSGAFIGITALLFLICLALIMKILPKRTOTETPRPRFSHTILDYI 540
 DB 481 DKKGLISTAFNSGAFIGITALLFLICLALIMKILPKRTOTETPRPRFSHTILDYI 540
 QY 541 NVVPTAGPLAQRNOKATNSPRTPLPGCAPSPESKKNOKKQYQLPSPEPKSSQAPES 600
 DB 541 NVVPTAGPLAQRNOKATNSPRTPLPGCAPSPESKKNOKKQYQLPSPEPKSSQAPES 600
 QY 601 QBSQELHLYATINFPQVRPRPRARMKPGTQADYAEVKFQ 639
 DB 601 QBSQELHLYATINFPQVRPRPRARMKPGTQADYAEVKFQ 639

RESULT 2

AA197543

ID AAY97543 standard; protein; 639 AA.

XX AAY97543;

XX AAY97543;

DT 12-FEB-2001 (first entry)

XX Human obesity protein binding protein-2 homologue #2.
 DE Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
 XX obesity-related disorder; therapy.
 KW Homo sapiens.
 XX WO200059942-A2.
 PN 12-OCT-2000.
 PD 22-MAR-2000; 2000WO-US006682.
 PF 02-APR-1999; 99US-0127667P.
 XX (ELIL) LILLY & CO ELI.
 PA Su EW, Wei J;
 PI WPI; 2000-664992/64.
 XX N-PSDB; AAA37848.
 DR New human obesity protein binding protein-2 homologue nucleic acids,
 PT polynucleotides and polypeptides useful for producing medicament for
 FT treating obesity and/or obesity-related disorders.
 XX Claim 9; Page 89-91; 92pp; English.
 CC This sequence is a human obesity protein binding protein-2 homologue (hOB
 -BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may
 be used for the manufacture of a medicament for the treatment of obesity
 and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful
 as probes or amplification primers in the detection, quantification or
 isolation of gene sequences or transcripts, for recombinant expression of
 hOB-BP2h polypeptides, as immunogens in the preparation and screening of
 antibodies, and in sense or antisense suppression of one or more hOB-BP2h
 genes or nucleic acids, host cell or tissue in vivo or in vitro.
 CC Antigenic epitope-bearing peptides and polypeptides are useful for
 CC raising or screening antibodies that specifically binds to the hOB-BP2h
 CC polypeptides

SQ Sequence 639 AA;

Query Match 100.0%; Score 3377; DB 3; Length 639;
 Best Local Similarity 100.0%; Pred. No. 2.3e-232;
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLPILLSLLGSGQAMDGFRFIRVQESVNVPEGLCISVPCSFSPRQDWTGTPAYGYW 60
 DB 1 MLLPILLSLLGSGQAMDGFRFIRVQESVNVPEGLCISVPCSFSPRQDWTGTPAYGYW 60
 QY 61 FKAVTTTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFVRV 120
 DB 61 FKAVTTTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFVRV 120
 QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSAQTVRLVAYAP 180
 DB 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSAQTVRLVAYAP 180
 QY 181 RDLVISISRDNTPALPEPQGNVPYILEAQKGQFLRLCAADSQPPATLSWLVQNRVLSS 240
 DB 181 RDLVISISRDNTPALPEPQGNVPYILEAQKGQFLRLCAADSQPPATLSWLVQNRVLSS 240
 QY 241 HPWGPRPLGLELPGVKGAGSGRVTCAENRIGSQORALDLSVQYPPENLRVWVSQANRTV 300
 DB 241 HPWGPRPLGLELPGVKGAGSGRVTCAENRIGSQORALDLSVQYPPENLRVWVSQANRTV 300
 QY 301 LENLNGTSLPVLGGQSLCIVCVTHSSPPARLSWTRQGVLSQPSQSDPGVLELPRVQVE 360
 DB 301 LENLNGTSLPVLGGQSLCIVCVTHSSPPARLSWTRQGVLSQPSQSDPGVLELPRVQVE 360
 QY 361 HEGEFTCHARHPLGSHVSLSVHYSPKILGPSCSWEAEGHLCSSQASAPSLRWL 420

Db 361 HEGEFTCHARHPLGSHVLSVSHYSPKILGPSCWEAEGHSCSSQASPAPSLRWL 420
Qy 421 GEELLEGNSQDSREVTSSAGPWANSSLSHGLSSGLRLRCRAWNVHGAQSGSILQLP 480
Db 421 GEELLEGNSQDSREVTSSAGPWANSSLSHGLSSGLRLRCRAWNVHGAQSGSILQLP 480
Qy 481 DKKGLISTAFNGAFLGIGITALLFLCLALIIMKILPKRRTQTTPRFRSHSTILDYI 540
Db 481 DKKGLISTAFNGAFLGIGITALLFLCLALIIMKILPKRRTQTTPRFRSHSTILDYI 540
Qy 541 NVVPTAGLAQRNOKATPNSPRTPPLPGAPSPESKKNOKKQYQLPSPPEKSTQAPES 600
Db 541 NVVPTAGLAQRNOKATPNSPRTPPLPGAPSPESKKNOKKQYQLPSPPEKSTQAPES 600
Qy 601 QESQELHYATLNFPGVRPPEARMKPGTQADYAEVKFQ 639
Db 601 QESQELHYATLNFPGVRPPEARMKPGTQADYAEVKFQ 639
RESULT 3
ID AAB25580
XX AAB25580 standard; protein; 639 AA.
AC AAB25580;
XX
DT 21-NOV-2000 (first entry)
DE CD33-like protein encoded by human secreted protein gene #5.
KW Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
KW antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
KW anticancer; vulnary; antiviral; antibacterial; antifungal;
KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
KW Crohn's disease; nephritis; hyperproliferative disorder;
KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
KW melanoma; lymphoma; wound healing; human.
XX
OS Homo sapiens.
XX
PN WO200029435-A1.
XX
PD 25-MAY-2000.
XX
PF 27-OCT-1999; 99WO-US025031.
XX
PR 28-OCT-1998; 98US-0105971P.
XX
PA (HUKA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
PI Greene JM;
XX
DR WPI; 2000-387742/33.
DR N-PSDB; AAA80610.
XX
PT Isolated nucleic acid molecules encoding human secreted proteins are used
PT for the prevention, amelioration and treatment of autoimmune,
PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
PT wounds, and infectious diseases.
XX
PS Claim 1; Fig 13A-C; 803pp; English.
XX
CC The present invention relates to 12 secreted human proteins and the
CC nucleotide sequences encoding them. The polynucleotide sequences given in
CC AAB25580-A80623 encode the 12 secreted protein sequences given in
CC AAB25576-B25593. The human secreted proteins have various activities
CC dependent on the tissues in which they are expressed. Examples of the
CC activities of the proteins include: immunosuppressant; anti-inflammatory;
CC antiarthritic; antirheumatic; dermatological; antiproliferative;
CC antiarteriosclerotic; anticancer; vulnary; antiviral; antibacterial;
CC and antifungal activity. The proteins, polypeptides, agonists and

CC antagonists may be used to treat prevent and/or diagnose various disease,
CC disorders and conditions examples of which include: immune disorders e.g.
CC Addison's disease, rheumatoid arthritis, dermatitis, and multiple
CC sclerosis; inflammatory disorders e.g. inflammatory bowel disease,
CC Crohn's disease and nephritis; hyperproliferative disorders such as
CC paraneoplasias and myeloplasia; cardiovascular disorders e.g. coronary
CC arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The
CC proteins and polynucleotide sequences may also be used in wound healing
CC and the treatment of infectious diseases. The human secreted protein gene
CC #5 and protein sequences are represented in sequences AAA80610 and
CC AAB25580. Sequences AAA80638-A80649 represent genes related to the
CC secreted protein genes
XX
SQ Sequence 639 AA;
Query Match 99.3%; Score 3354; DB 3; Length 639;
Best Local Similarity 99.5%; Pred. No. 1e-230;
Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MLLPLLLSLLGGSQAMGRFWIRVOESVMVPEGLCISVPCSFSPQDMGTSTPAYGW 60
Db 1 MLLPLLLSLLGGSQAMGRFWIRVOESVMVPEGLCISVPCSFSPQDMGTSTPAYGW 60
Qy 61 FKAVTETTKGAPVATNHQREVEVMSRGRFQLTGDPAKGNCSLVIRDAQMDQESQYFFRV 120
Db 61 FKAVTETTKGAPVATNHQREVEVMSRGRFQLTGDPAKGNCSLVIRDAQMDQESQYFFRV 120
Qy 121 ERGSYRVNPMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSRKGVSQARTVRLVAYAP 180
Db 121 ERGSYRVNPMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSRKGVSQARTVRLVAYAP 180
Qy 181 RDLVISISRNTTALPEPOQGNVPLYEAQKQFRLLLCAADSPATLSWVLQNRVLSSS 240
Db 181 RDLVISISRNTTALPEPOQGNVPLYEAQKQFRLLLCAADSPATLSWVLQNRVLSSS 240
Qy 241 HPWGPRPLGLEPLGVKAGSGRVTCAENRPLGSQLALDLSVQYPPENLKVMSQANRTV 300
Db 241 HPWGPRPLGLEPLGVKAGSGRVTCAENRPLGSQLALDLSVQYPPENLKVMSQANRTV 300
Qy 301 LENLNGTSLPVEGOSLCVTHSSPPARLSWTORGOVLSPOSDPGVLELPRVOVE 360
Db 301 LENLNGTSLPVEGOSLCVTHSSPPARLSWTORGOVLSPOSDPGVLELPRVOVE 360
Qy 361 HEGEFTCHARHPLGSHVLSVSHYSPKILGPSCWEAEGHSCSSQASPAPSLRWL 420
Db 361 HEGEFTCHARHPLGSHVLSVSHYSPKILGPSCWEAEGHSCSSQASPAPSLRWL 420
Qy 421 GEELLEGNSQDSREVTSSAGPWANSSLSHGLSSGLRLRCRAWNVHGAQSGSILQLP 480
Db 421 GEELLEGNSQDSREVTSSAGPWANSSLSHGLSSGLRLRCRAWNVHGAQSGSILQLP 480
Qy 481 DKKGLISTAFNGAFLGIGITALLFLCLALIIMKILPKRRTQTTPRFRSHSTILDYI 540
Db 481 DKKGLISTAFNGAFLGIGITALLFLCLALIIMKILPKRRTQTTPRFRSHSTILDYI 540
Qy 541 NVVPTAGLAQRNOKATPNSPRTPPLPGAPSPESKKNOKKQYQLPSPPEKSTQAPES 600
Db 541 NVVPTAGLAQRNOKATPNSPRTPPLPGAPSPESKKNOKKQYQLPSPPEKSTQAPES 600
Qy 601 QESQELHYATLNFPGVRPPEARMKPGTQADYAEVKFQ 639
Db 601 QESQELHYATLNFPGVRPPEARMKPGTQADYAEVKFQ 639
RESULT 4
ADA27052
ID ADA27052 standard; protein; 639 AA.
XX
AC ADA27052;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human novel secreted protein from cDNA HDPCL05 #1.

XX cytotatic; antiinflammatory; immunomodulator; neuroprotective;
 XX hemostatic; gene therapy; cancer; inflammation; immune disorder;
 XX neurological disorder; blood clotting disorder; food additive;
 XX preservative; human; secreted protein.

XX Homo sapiens.

XX US200305231-A1.

XX 20-MAR-2003.

XX 29-OCT-2001; 2001US-00984130.

XX 28-OCT-1998; 98US-0105971P.

XX 27-OCT-1999; 99WO-05025031.

XX 19-APR-2000; 2000US-0198407P.

XX 30-OCT-2000; 2000US-0243792P.

XX 18-APR-2001; 2001US-00836353.

XX (NLIJ/) NI J.

XX (YOUNG/) YOUNG P E.

XX (KENN/) KENNY J J.

XX (OLSE/) OLSEN H S.

XX (MOOR/) MOORE P A.

XX (WEIY/) WEI Y.

XX (GREE/) GREENE J M.

XX (RUBE/) RUBEN S M.

XX (LIUD/) LIU D.

XX (CROC/) CROCKER P R.

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XX Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 XX Ruben SM, Liu D, Crocker PR;

XX WPI: 2003-567103/53.

XX N-PSDB; ADA27034.

XX New human secreted nucleic acid molecules and polypeptides, useful for
 XX preventing, treating, or ameliorating a medical condition, such as
 XX cancer, inflammation, immune disorders, neurological and blood clotting
 XX disorders.

XX Claim 11; Fig 13; 454pp; English.

XX The invention relates to an isolated nucleic molecule that is at least
 XX 95% identical to 18 human cDNA sequences representing 12 novel genes
 XX encoding secreted proteins or a polynucleotide fragment of the cDNA
 XX sequence contained in American Type Culture Collection (ATCC) deposit No.
 XX defined in the specification, its species homologue, a variant or allelic
 XX variant of the polynucleotide having a polynucleotide capable of
 XX hybridising under conditions the polynucleotide, where the polynucleotide
 XX does not hybridise under stringent conditions to a nucleic acid molecule
 XX having a nucleotide sequence of only A or T residues. Also included are
 XX recombinant vectors, host cells (for producing the polypeptide), the
 XX secreted polypeptide (comprising a sequence that is at least 95%
 XX identical to a polypeptide fragment: domain, epitope, full-length
 XX protein, variant, allelic variant or species homologue), antibodies that
 XX specifically bind to the polypeptides, diagnosing, treating, preventing
 XX or ameliorating a medical condition by administering the polynucleotide
 XX or the polypeptide, the gene corresponding to the cDNA sequence and
 XX identifying an activity in a biological assay (by expressing the cDNA
 XX sequence in a cell, isolating the supernatant, and detecting an activity
 XX in a biological assay and identifying the protein in the supernatant
 XX having the activity). The polypeptides, nucleic acids and antibodies are
 XX useful for diagnosing a pathological condition or a susceptibility to a
 XX pathological condition, for preventing, treating, or ameliorating a
 XX medical condition, such as cancer, inflammation and other immune
 XX disorders, neurological and blood clotting disorders (many examples are
 XX given in the specification). The nucleic acids are also useful for
 XX chromosome identification, radiation hybrid mapping or long-range
 XX restriction mapping. The polypeptides and antibodies are useful for
 XX providing immunological probes for differential identification of the
 XX tissues immunohistochemistry assays. The polypeptide, polynucleotide,

CC agonist or antagonist may also be used as a food additive or preservative
 CC to increase or decrease storage capabilities, fat content or other
 CC nutritional components. The present is a secreted protein of the
 CC invention.

XX SQ Sequence 639 AA;

XX Query Match 99.3%; Score 3354; DB 6; Length 639;

XX Best Local Similarity 99.5%; Pred. No. 1e-230;

XX Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLPILLSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFYPRQDMTGSTPAYGW 60

DB 1 MLLPILLSLLGGSQAMDGRFWIRVQESVMVPEACDISVPCSFYPRQDMTGSTPAYGW 60

QY 61 FKAVTETTKGAPVATNHQREVEVMSRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFVRV 120

DB 61 FKAVTETTKGAPVATNHQREVEVMSRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFVRV 120

QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPQDHTDLTCHVDFSRKGVSAQRTVLRLVAYAP 180

DB 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPQDHTDLTCHVDFSRKGVSAQRTVLRLVAYAP 180

QY 181 RDLVISISRDNTPALBPQPGNVPIYLEAKGQFLRLCAADSOFPATLSWLNQRLVSSS 240

DB 181 RDLVISISRDNTPALBPQPGNVPIYLEAKGQFLRLCAADSOFPATLSWLNQRLVSSS 240

QY 241 HPWGPRPLGLELPGVKGADSGRYTCRAENRLGSOQALDLSVOYPPENLRVMVSOANRTV 300

DB 241 HPWGPRPLGLELPGVKGADSGRYTCRAENRLGSOQALDLSVOYPPENLRVMVSOANRTV 300

QY 301 LENLNGTSLPVLLEGOSLCLVCVTHSSPPARLSWTOGQVLSQSPSDPGVLELPRVQVE 360

DB 301 LENLNGTSLPVLLEGOSLCLVCVTHSSPPARLSWTOGQVLSQSPSDPGVLELPRVQVE 360

QY 361 HEGEFTCHASHPLGSOHVLSLSVHYSPKLLGPSCSWEAEGHLCSSQASPAAPSLRWL 420

DB 361 HEGEFTCHASHPLGSOHVLSLSVHYSPKLLGPSCSWEAEGHLCSSQASPAAPSLRWL 420

QY 421 GEBLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAVNWHGAQSGSLQLP 480

DB 421 GEBLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAVNWHGAQSGSLQLP 480

QY 481 DKXGLISTAFSNGAFLEGITALLFLCLALINKILPKRTQTETPRPFSRHSHTILDYI 540

DB 481 DKXGLISTAFSNGAFLEGITALLFLCLALINKILPKRTQTETPRPFSRHSHTILDYI 540

QY 541 NVVPTAGPLAOKENQKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPEPKSSTQAPES 600

DB 541 NVVPTAGPLAOKENQKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPEPKSSTQAPES 600

QY 601 QESQELHYATLNFPGVRRPPEARMKPGTQADYAEVKFQ 639

DB 601 QESQELHYATLNFPGVRRPPEARMKPGTQADYAEVKFQ 639

RESULT 5

ID ADE86582 standard; protein: 639 AA.

XX ADE86582;

XX 29-JAN-2004 (first entry)

XX DE Novel human secreted protein #5.

XX human; secreted protein; cancer; liver disorder; hepatitis;

XX neural disorder; Alzheimer's disease.

XX Homo sapiens.

XX US2003129685-A1.

XX

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PD 10-JUL-2003.
XX
XX 18-APR-2001; 2001US-00836353.
XX
XX 28-OCT-1998; 98US-0105971P.
XX 27-OCT-1999; 99WO-US025031.
XX 19-APR-2000; 2000US-0198407P.
XX
XX (NIJ/) NI J.
XX (YOUNG/) YOUNG P E.
XX (Kenny/) KENNY J J.
XX (OLSEN/) OLSEN H S.
XX (MOORE/) MOORE P A.
XX (WEI/) WEI Y.
XX (GREENE/) GREENE J M.
XX (RUBEN/) RUBEN S M.
XX
XX Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
PI Ruben SM;
XX
XX WPI; 2004-020335/02.
XX N-PSDB; ADB86564.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g. cancer,
PT liver disorders or neural disorders.
XX
XX Claim 11; SEQ ID NO 33; 380pp; English.
XX
XX The invention relates to an isolated nucleic acid sequence, or its
CC allelic variant, a fragment of the cDNA sequence, or its fragment,
CC domain, epitope or species homologue. The nucleic acid is useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition e.g., cancer, liver disorders such as hepatitis or neural
CC disorders such as Alzheimer's disease. The present sequence represents
CC the amino acid sequence of a novel human secreted protein.
XX
XX Sequence 639 AA;
XX
Query Match 99.3%; Score 3354; DB 8; Length 639;
Best Local Similarity 99.5%; Pred. No. 1e-230;
Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MLLPLLSSLLGSGQAMDGFRFIRVOESVWVPEGLCISVPCFSYPRQDWTGSTPAYGYW 60
DB 1 MLLPLLSSLLGSGQAMDGFRFIRVOESVWVPEACDISVPCFSYPRQDWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNHQREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
DB 61 FKAVTETTKGAPVATNHQREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
QY 121 ERGSYVRVNFMDGPFVKTVLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAVAP 180
DB 121 ERGSYVRVNFMDGPFVKTVLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAVAP 180
QY 181 RDLVISISRDNTPALEPQGNVPVLEAKQGFRLCAADSPATLSWLNQNRVLSSS 240
DB 181 RDLVISISRDNTPALEPQGNVPVLEAKQGFRLCAADSPATLSWLNQNRVLSSS 240
QY 241 HPWGRPRGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVWVSQANVT 300
DB 241 HPWGRPRGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVWVSQANVT 300
QY 301 LENLNGTSLPVLGGQSLCLVCVTHSSPPARLSWTQRGQVLSFSPQSPDFGVLELPRVQVE 360
DB 301 LENLNGTSLPVLGGQSLCLVCVTHSSPPARLSWTQRGQVLSFSPQSPDFGVLELPRVQVE 360
QY 361 HGEFTCHAPHLGSOHVSLSVHYSKLLGFCSSWEAGLHCSCSSQASPSLRWL 420
DB 361 HGEFTCHAPHLGSOHVSLSVHYSKLLGFCSSWEAGLHCSCSSQASPSLRWL 420
QY 421 GBELEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRCEANVHGAQSGSILQLP 480
DB 421 GBELEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRCEANVHGAQSGSILQLP 480
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Db 421 GBELEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRCEANVHGAQSGSILQLP 480
QY 481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRETQTETPRPFRSHSTILDYI 540
DB 481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRETQTETPRPFRSHSTILDYI 540
QY 541 NVVPTAGPLAQNCKATPNSPRTFPPGAPSPESKKNQKKQYQLSPFPFKSTQAPES 600
DB 541 NVVPTAGPLAQNCKATPNSPRTFPPGAPSPESKKNQKKQYQLSPFPFKSTQAPES 600
QY 601 QESQELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 639
DB 601 QESQELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 639
XX
XX AAU87087 standard; protein; 697 AA.
XX
XX AAU87087;
XX
XX 05-JUN-2002 (first entry)
XX
XX Sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-3.
XX
XX Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
XX immune system disease; leukaemia; allergy; inflammatory disease;
XX tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
XX psoriasis; rheumatoid arthritis; conjunctivitis.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO200208257-A2.
XX
XX 31-JAN-2002.
XX
XX 20-JUL-2001; 2001WO-US023082.
XX
XX 21-JUL-2000; 2000US-0220139P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Longphre M, Chang H, Whitney G;
XX
XX WPI; 2002-241565/29.
XX
XX N-PSDB; ABK43373.
XX
XX Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
XX molecules useful for treating immune system diseases such as asthma,
XX leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
XX
XX Example 11; Fig 6; 209pp; English.
XX
XX The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
XX related lectin) protein (I). Pharmaceutical compositions comprising (I)
XX are useful for treating immune system diseases such as asthma, leukaemia
XX or other allergic or inflammatory diseases. Extracellular domains of (I)
XX represent potential markers for screening, diagnosis, prognosis, follow-
XX up assays, and imaging methods. (I) is useful as a target for drugs which
XX inhibit inflammation, tissue damage and remodeling in asthma, and
XX inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
XX disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
XX also useful for monitoring the course of disease or disorders, and for
XX identifying agents that bind with and/or modulate the biological activity
XX of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
XX useful in diagnosis and/or prognosis methods, and to detect the presence
XX and/or amount of SIGLEC-BMS nucleoside sequences and/or SIGLEC-BMS
XX proteins in a biological sample. (II) are useful as nucleic acid probes
XX are useful for screening genomic library to isolate a genomic clone of
XX SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
XX diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
XX The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
```

CC expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
CC AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
CC invention
XX
XX
XX Sequence 697 AA;
XX
XX
XX Query Match 98.8%; Score 3338; DB 5; Length 697;
XX Best Local Similarity 91.7%; Pred. No. 1.6e-229;
XX Matches 639; Conservative 0; Mismatches 0; Indels 59; Gaps 1;
XX
XX 1 MLLPLLSSLLGSGQAMDRGFWIRVQESVWVPEGLCISVPCFSYPRQDWTGSTAYGW 60
XX
XX 1 MLLPLLSSLLGSGQAMDRGFWIRVQESVWVPEGLCISVPCFSYPRQDWTGSTAYGW 60
XX
XX 61 FKAVTETTKGAPVATNHQREVEVMSVTRGRFQLTGDPKAGNCSLVIRDAQMQDESQVFRV 120
XX
XX 61 FKAVTETTKGAPVATNHQREVEVMSVTRGRFQLTGDPKAGNCSLVIRDAQMQDESQVFRV 120
XX
XX 121 ERGSYVRYNPMNDGFFLKVT-----VLSFTRPDQDHTDLTCHVDFSRKGVSAQRTVRLVAYARD 140
XX
XX 121 ERGSYVRYNPMNDGFFLKVT-----VLSFTRPDQDHTDLTCHVDFSRKGVSAQRTVRLVAYARD 140
XX
XX 141 -----VLSFTRPDQDHTDLTCHVDFSRKGVSAQRTVRLVAYARD 180
XX
XX 181 TGAALSSQGTFTTSFHSVLSFTRPDQDHTDLTCHVDFSRKGVSAQRTVRLVAYARD 240
XX
XX 183 LVISISRDNTPALEPQFGNVPLYEAQKQFLRLCAADSQPPATLSWVLQNRVLSSHP 242
XX
XX 241 LVISISRDNTPALEPQFGNVPLYEAQKQFLRLCAADSQPPATLSWVLQNRVLSSHP 300
XX
XX 243 WGRPRPLGLELPGVKAGDSGRYTCRAENRLGSGQALDLSVQYPPENLRVWVQANRTVLE 302
XX
XX 301 WGRPRPLGLELPGVKAGDSGRYTCRAENRLGSGQALDLSVQYPPENLRVWVQANRTVLE 360
XX
XX 303 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQGVLSPPQSDPGVLELPRVQVEHE 362
XX
XX 361 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQGVLSPPQSDPGVLELPRVQVEHE 420
XX
XX 363 GEPTCHARPLGSHQVSLVSHVSPKLLGPGSCWEAGLHSCSQAAPSLRWLGE 422
XX
XX 421 GEPTCHARPLGSHQVSLVSHVSPKLLGPGSCWEAGLHSCSQAAPSLRWLGE 480
XX
XX 423 ELLEGNSDSDSRVPTSSAGPWANSSLSHGLSGSLRRCANVHGAQSSILQLPDK 482
XX
XX 481 ELLEGNSDSDSRVPTSSAGPWANSSLSHGLSGSLRRCANVHGAQSSILQLPDK 540
XX
XX 483 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRFRSRHSTILDYINV 542
XX
XX 541 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRFRSRHSTILDYINV 600
XX
XX 543 VPTAGPLAKRQKATPNSPRLPLPGAPSPSKNKKQYQLPFPPEKSTQAPESQE 602
XX
XX 601 VPTAGPLAKRQKATPNSPRLPLPGAPSPSKNKKQYQLPFPPEKSTQAPESQE 660
XX
XX 603 SQBELHYATLNPFGVPRPEARMKPKTQADYAEVFKQ 639
XX
XX 661 SQBELHYATLNPFGVPRPEARMKPKTQADYAEVFKQ 697
XX

RESULT 7
IDA27153
ID ADA27153 standard; protein; 697 AA.

XX ADA27153;

XX ADA27153; (first entry)

XX DE Human novel secreted protein from cDNA HDPCC05 #2.

XX KW cytostatic; antiinflammatory; immunomodulator; neuroprotective;

XX KW hemostatic; gene therapy; cancer; inflammation; immune disorder;

XX KW neurological disorder; blood clotting disorder; food additive;

XX KW preservative; human; secreted protein.

XX Homo sapiens.
XX US200305231-A1.
XX 20-MAR-2003.
XX 29-OCT-2001; 2001US-06984130.
XX 28-OCT-1998; 98US-0105971P.
XX 27-OCT-1999; 99WO-US025031.
XX 19-APR-2000; 2000US-0198407P.
XX 30-OCT-2000; 2000US-0243792P.
XX 18-APR-2001; 2001US-00836353.
XX (NIJJ/) NI J.
XX (YOUN/) YOUNG P E.
XX (KEND/) KENNY J J.
XX (OLSE/) OLSEN H S.
XX (MOOR/) MOORE P A.
XX (WEIY/) WEI Y.
XX (GREE/) GREENE J M.
XX (RUBE/) RUBEN S M.
XX (LIUD/) LIU D.
XX (CROC/) CROCKER P R.
XX NI J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
XX Ruben SM, Liu D, Crocker PR;
XX MPI: 2003-567103/53.
XX N-PSDB; ADA27152.
XX
XX New human secreted nucleic acid molecules and polypeptides, useful for
XX preventing, treating, or ameliorating a medical condition, such as
XX cancer, inflammation, immune disorders, neurological and blood clotting
XX disorders.
XX Claim 11; Page 383-385; 454pp; English.

The invention relates to an isolated nucleic molecule that is at least 95% identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polynucleotide fragment of the cDNA sequence contained in American Type Culture Collection (ATCC) deposit No. defined in the specification, its species homologue, a variant or allelic variant of the polynucleotide having a polynucleotide capable of hybridising under conditions the polynucleotide, where the polynucleotide does not hybridise under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polypeptide), the secreted polypeptide (comprising a sequence that is at least 95% identical to a polypeptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polypeptides, diagnosing, treating, preventing or ameliorating a medical condition by administering the polynucleotide or the polypeptide, the gene corresponding to the cDNA sequence and identifying an activity in a biological assay (by expressing the cDNA sequence in a cell, isolating the supernatant, and detecting an activity in a biological assay and identifying the protein in the supernatant having the activity). The polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders (many examples are given in the specification). The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other nutritional components. The present is a secreted protein of the invention.

```
SQ      Sequence 697 AA;
Query Match      98.7%; Score 3334; DB 6; Length 697;
Best Local Similarity 91.5%; Pred. No. 3e-229;
Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY      1 MLPLLSLLGSGQAMDGFWIRVOESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
DQ      1 MLPLLSLLGSGQAMDGFWIRVOESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
QY      61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
DQ      61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
QY      121 ERGSYRYNPMNDGFLKVT----- 140
DQ      121 ERGSYRYNPMNDGFLKVT----- 140
QY      141 -----VLSFTPRQDHTNLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182
DQ      181 TGAALSSQGTPTTSHFSVLTSTPRQDHTNLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
QY      183 LVISIRSDNTPALEPOQGNVPEYLAQKQFLLELCAADSQPPATLSWYLNQNRVLSSSH 242
DQ      241 LVISIRSDNTPALEPOQGNVPEYLAQKQFLLELCAADSQPPATLSWYLNQNRVLSSSH 300
QY      243 WGPRLPLGLPGVAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVSOANETVLE 302
DQ      301 WGPRLPLGLPGVAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVSOANETVLE 360
QY      303 NLNGNTSLVLEGGQSLCLVCTHSSPPARLSWTQGVLSPPQSDPGVLELPRVQVEHE 362
DQ      361 NLNGNTSLVLEGGQSLCLVCTHSSPPARLSWTQGVLSPPQSDPGVLELPRVQVEHE 420
QY      363 GEFTCHARPLGSOHVSLSVHYSPKLLGPSCSWEAELHSCSSQASAPSLRWLGE 422
DQ      421 GEFTCHARPLGSOHVSLSVHYSPKLLGPSCSWEAELHSCSSQASAPSLRWLGE 480
QY      423 ELLEGNSODSPVTPSSAGPWANGLSLHGLSSGLRLRCBANVHGAQSGSILQLPDK 482
DQ      481 ELLEGNSODSPVTPSSAGPWANGLSLHGLSSGLRLRCBANVHGAQSGSILQLPDK 540
QY      483 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRRTQTTPRPSRHSHTILDYINV 542
DQ      541 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRRTQTTPRPSRHSHTILDYINV 600
QY      543 VTAGPLAQRNOKATNSPRTPLPAGPSPESKKNQKQYOLPSPFPKSTQAPESQE 602
DQ      601 VTAGPLAQRNOKATNSPRTPLPAGPSPESKKNQKQYOLPSPFPKSTQAPESQE 660
QY      603 SOEELHYATLNPFGVRRPEARMKGTQADYAEVKFQ 639
DQ      661 SOEELHYATLNPFGVRRPEARMKGTQADYAEVKFQ 697

RESULT 8
ADD26582
ID      ADD26582 standard; protein; 697 AA.
XX
AC      ADD26582;
XX
DT      15-JAN-2004 (first entry)
XX
DE      Siglec-10 amino acid sequence SEQ ID NO:7.
XX
KW      human; cell surface protein; immunoglobulin; BGS-19; cytostatic;
KW      gynaecological; immunosuppressive; antiinflammatory; antiasthmatic;
KW      antidiabetic; dermatological; gene therapy.
XX
OS      Homo sapiens.
XX
PN      WC02003083078-A2.
XX
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PD      09-OCT-2003.
XX
PF      28-MAR-2003; 2003WO-US009676.
XX
PR      28-MAR-2002; 2002US-0368422P.
XX
PA      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI      Lee LM, Feder JN, Siemers NQ, Wu S, Chen J;
XX
WPI, 2003-804052/75.
XX
New isolated nucleic acid molecule encoding BGS-19 polypeptides, useful
for preventing, treating or ameliorating a medical condition, such as a
PT disorder related to aberrant immunoglobulin cell surface receptor
PT activity.
XX
Example 1; SEQ ID NO 7; 224pp; English.
XX
The present invention describes human cell surface protein with
immunoglobulin folds, designated BGS-19 (I). (i) has cytosolic,
gynaecological, immunosuppressive, antiinflammatory, antiasthmatic,
antidiabetic and dermatological activities, and can be used in gene
therapy. (ii) can be used for preventing, treating or ameliorating a
medical condition, such as a disorder related to aberrant immunoglobulin
cell surface receptor activity; a cellular adhesion disorder; a disorder
related to hyper- or hypo-immunoglobulin receptor activity; a disorder
related to aberrant signal transduction; a reproductive disorder; a
female reproductive disorder; an ovarian disorder; ovarian cancer; a
dysfunctional uterine bleeding; amenorrhoea; primary dysmenorrhoea;
sexual dysfunction; infertility; pelvic inflammatory disease;
endometriosis; placental aromatase deficiency; premature menopause;
placental dysfunction; hormone deficiency; oestrogen deficiency; aberrant
androgen metabolism; aberrant onset of female puberty; aberrant showing
of female primary sexual characteristics; aberrant showing of female
secondary sexual characteristics; precocious puberty; precocious
pseudopuberty; incomplete isosexual precocity; premature thelarche;
premature adrenarche; premature pubarche; polycystic ovarian disease;
aberrant ovarian cycle; menorrhagia; metrorrhagia; menometrorrhagia;
dysmenorrhoea; hypomenorrhoea; polymenorrhoea; dysfunctional uterine
bleeding; resistant-ovary syndrome; hermaphroditism; immune disorders;
inflammatory disorders; arthritis; asthma; immunodeficiency diseases such
as AIDS; leukaemia; rheumatoid arthritis; granulomatous disease;
inflammatory bowel disease; sepsis; acne; neutropenia; neutrophilia;
psoriasis; hypersensitivities; such as T-cell mediated cytotoxicity;
immune reactions to transplanted organs and tissues; such as host-versus-
graft and graft-versus-host diseases; or autoimmunity disorders;
autoimmune infertility; Addison's disease; haemolytic anaemia;
antiphospholipid syndrome; rheumatoid arthritis; dermatitis; allergic
encephalomyelitis; glomerulonephritis; Goodpasture's Syndrome; Graves'
Disease; Multiple Sclerosis; Myasthenia Gravis; Neuritis; Ophthalmia;
Bullous Pemphigoid; Pemphigus; Polyendocrinopathies; Purpura; Reiter's
Disease; Stiff-Man Syndrome; Autoimmune thyroiditis; Systemic Lupus
Erythematosus; Autoimmune Pulmonary Inflammation; Guillain-Barre Syndrome
; insulin dependent diabetes mellitus; autoimmune inflammatory eye
disease; lens tissue injury; demyelination; systemic lupus erythematosus;
drug induced haemolytic anaemia; rheumatoid arthritis; Sjogren's disease;
and scleroderma. The present sequence is given in comparison with BGS-19
in the present invention.
XX
SQ      Sequence 697 AA;
```

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Query Match      98.7%; Score 3334; DB 7; Length 697;
Best Local Similarity 91.5%; Pred. No. 3e-229;
Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY      1 MLPLLSLLGSGQAMDGFWIRVOESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
DQ      1 MLPLLSLLGSGQAMDGFWIRVOESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
QY      61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
DQ      61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
```

121 ERGSYVRYNFMNDGFLFKVT----- 140
 121 ERGSYVRYNFMNDGFLFKVTALTQKPDVYIPETLPGQPVTVICVFNWAFECPPPSFW 180
 141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAVAPRD 182
 181 TGAALSSQGTPTTSHFVLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAVAPRD 240
 183 LVTSISRDNTPALEPQPGNVVYLEAKGQFRLCAADSPATLSWLVQNRVLSSSH 242
 241 LVTSISRDNTPALEPQPGNVVYLEAKGQFRLCAADSPATLSWLVQNRVLSSSH 300
 243 WGRPRPLGLELPVLEQSGSLVCHVTHSSPPARLSWTORGQVLSPPQDPGVLELPRVQVEHE 362
 301 WGRPRPLGLELPVLEQSGSLVCHVTHSSPPARLSWTORGQVLSPPQDPGVLELPRVQVEHE 360
 303 NLNGTSLPVLEQSGSLVCHVTHSSPPARLSWTORGQVLSPPQDPGVLELPRVQVEHE 362
 361 NLNGTSLPVLEQSGSLVCHVTHSSPPARLSWTORGQVLSPPQDPGVLELPRVQVEHE 420
 363 GEFTCHARHPLGSHVLSVHYSPKLLGPGSCWEAGLHCSCSSQASPAFLRWLGE 422
 421 GEFTCHARHPLGSHVLSVHYSPKLLGPGSCWEAGLHCSCSSQASPAFLRWLGE 480
 423 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCBAMNVHGAQSGSILQLPDK 482
 481 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCBAMNVHGAQSGSILQLPDK 540
 483 KGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRFRFSHSTILDYINV 542
 541 KGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRFRFSHSTILDYINV 600
 543 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKXKQKQYQLPSPPEKSTQAPESQE 602
 601 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKXKQKQYQLPSPPEKSTQAPESQE 660
 603 SOBELHYATLNFPGVPRPEARMEKGTQADYAEVKFQ 639
 661 SOBELHYATLNFPGVPRPEARMEKGTQADYAEVKFQ 697

RESULT 9

AD137010
 ID AD137010 standard; protein; 697 AA.

XX AC AD137010;

XX DT 22-APR-2004 (first entry)

XX DE Novel human secreted and transmembrane protein PRO 71236.

XX human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neurotrophic factor; hormone; cell receptor;
 KW receptor-ligand interaction; cytoskeletal; chondrocyte; tumour.

XX CS Homo sapiens.

XX PN WO2004004649-A2.

XX PD 15-JAN-2004.

XX PR 08-JUL-2003; 2003WO-US021083.

XX PR 08-JUL-2002; 2002US-0394485P.

XX PA (GETH) GENENTECH INC.

XX PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld J, Wood W, Wu T;

XX PI WPI; 2004-142912/14.

XX DR

DR N-PSDB; AD137009.

XX PS Claim 10; SEQ ID NO 10; 118pp; English.

XX CC This invention relates to novel nucleic acids encoding human PRO secreted
 CC and transmembrane proteins. Extracellular proteins play important roles
 CC in the formation, differentiation and maintenance of multicellular
 CC organisms. The fate of many individual cells (for example proliferation,
 CC migration or differentiation) is typically governed by information
 CC received from other cells and the immediate environment. The information
 CC is often transmitted by secreted polypeptides (for example mitogenic
 CC factors, survival factors, cytotoxic factors, differentiation factors,
 CC neurotrophic factors and hormones) which are received and interpreted by diverse
 CC cell receptors or membrane bound proteins. These membrane bound proteins
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such
 CC as in the blocking of receptor-ligand interactions. The current invention
 CC provides the amino acid sequences of novel human membrane bound receptors
 CC and proteins, along with the cDNA sequences encoding them. The novel
 CC proteins of the invention may have cytoskeletal activities through the
 CC stimulation of chondrocytes. The nucleic acids of the invention may be
 CC useful for the manufacture of a medicament for diagnosing or treating a
 CC tumour in a mammal. In addition, they may be useful for measuring or
 CC detecting the expression of a tumour associated gene. The present
 CC sequence is the amino acid sequence of a human PRO protein of the
 CC invention.

XX SQ Sequence 697 AA;

Query Match 98.7%; Score 3334; DB 8; Length 697;
 Best Local Similarity 91.5%; Pred. No. 3e-229;

Matches 538; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY 1 MLLPLLSLLSGSQADGDFWIRVQESVNVVPGCLCISVPCSYPRQDTGTTPAYGW 60

DB 1 MLLPLLSLLSGSQADGDFWIRVQESVNVVPGCLCISVPCSYPRQDTGTTPAYGW 60

QY 61 FKAVTETTKGAPVATNHQSRVEMSTGRFQLTGDPKAGNCSLVIRDAQMDSSQYFFRV 120

DB 61 FKAVTETTKGAPVATNHQSRVEMSTGRFQLTGDPKAGNCSLVIRDAQMDSSQYFFRV 120

QY 121 ERGSYVRYNFMNDGFFLKVT----- 140

DB 121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLPGQPVTVICVFNWAFECPPPSFW 180

QY 141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAVAPRD 182

DB 181 TGAALSSQGTPTTSHFVLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAVAPRD 240

QY 183 LVTSISRDNTPALEPQPGNVVYLEAKGQFRLCAADSPATLSWLVQNRVLSSSH 242

DB 241 LVTSISRDNTPALEPQPGNVVYLEAKGQFRLCAADSPATLSWLVQNRVLSSSH 300

QY 243 WGRPRPLGLELPVLEQSGSLVCHVTHSSPPARLSWTORGQVLSPPQDPGVLELPRVQVEHE 302

DB 301 WGRPRPLGLELPVLEQSGSLVCHVTHSSPPARLSWTORGQVLSPPQDPGVLELPRVQVEHE 360

QY 303 NLNGTSLPVLEQSGSLVCHVTHSSPPARLSWTORGQVLSPPQDPGVLELPRVQVEHE 362

DB 361 NLNGTSLPVLEQSGSLVCHVTHSSPPARLSWTORGQVLSPPQDPGVLELPRVQVEHE 420

QY 363 GEFTCHARHPLGSHVLSVHYSPKLLGPGSCWEAGLHCSCSSQASPAFLRWLGE 422

DB 421 GEFTCHARHPLGSHVLSVHYSPKLLGPGSCWEAGLHCSCSSQASPAFLRWLGE 480

QY 423 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCBAMNVHGAQSGSILQLPDK 482

DB 481 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCBAMNVHGAQSGSILQLPDK 540

QY 483 KGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRFRFSHSTILDYINV 542

DB 541 KGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRFRFSHSTILDYINV 600

QY 543 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKXKQKQYQLPSPPEKSTQAPESQE 602

pi Longphre M, Chang H, Whitney G;
xx WPI; 2002-241565/29.
xx N-PSDB; ABK43361.
xx Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
xx molecules useful for treating immune system diseases such as asthma,
xx leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
xx Claim 5; Fig 3B; 209pp; English.
xx The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
xx related lectin) protein (I). Pharmaceutical compositions comprising (I)
xx are useful for treating immune system diseases such as asthma, leukaemia
xx or other allergic or inflammatory diseases. Extracellular domains of (I)
xx represent potential markers for screening, diagnosis, prognosis, follow-
xx up assays, and imaging methods. (I) is useful as a target for drugs which
xx inhibit inflammation, tissue damage and remodeling in asthma, and
xx inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
xx disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
xx also useful for monitoring the course of disease or disorders, and for
xx identifying agents that bind with and/or modulate the biological activity
xx of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
xx useful in diagnosis and/or prognosis methods, and to detect the presence
xx and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS
xx proteins in a biological sample. (II) are useful as nucleic acid probes
xx are useful for screening genomic library to isolate a genomic clone of
xx SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
xx diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
xx The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
xx expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
xx AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
xx invention
xx
xx Sequence 622 AA;

Query Match 97.7%; Score 3299; DB 5; Length 622;
Best Local Similarity 100.0%; Pred. No. 8.1e-227;
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
18 DGRFWIRVQESVWVPGLCISVPCSFSPQDWTGSTPAYGVWFAVETTTKGAPVATNH 77
1 DGRFWIRVQESVWVPGLCISVPCSFSPQDWTGSTPAYGVWFAVETTTKGAPVATNH 60
78 QSRVEMSTRGRQLTGDPAKNCISVIRDAQMDQESQYFFRVERGSGYVYVNFMDGFPL 137
61 QSRVEMSTRGRQLTGDPAKNCISVIRDAQMDQESQYFFRVERGSGYVYVNFMDGFPL 120
138 KTVLSFTPRPDHNTDLTCHVDFSRKGSACQTVRLRVAYAPRDLVISRDNTPALEP 197
121 KTVLSFTPRPDHNTDLTCHVDFSRKGSACQTVRLRVAYAPRDLVISRDNTPALEP 180
198 QPQGNVPYLEAQKGQFLRLLCADSPATLSVNLQNRVLSSSHHPGPRPLGLEPGVKA 257
181 QPQGNVPYLEAQKGQFLRLLCADSPATLSVNLQNRVLSSSHHPGPRPLGLEPGVKA 240
258 GDSGRVTCRAENRGLSCQALDLSVQYPPENRVMSQANRVLENLNGTSLPVLGQS 317
241 GDSGRVTCRAENRGLSCQALDLSVQYPPENRVMSQANRVLENLNGTSLPVLGQS 300
318 LCVVCTHSSPPARLSWTORGQVLSQSDPQVLELPRVQVEHEGEFTCHARHPLGSGH 377
301 LCVVCTHSSPPARLSWTORGQVLSQSDPQVLELPRVQVEHEGEFTCHARHPLGSGH 360
378 VLSLSVHVSPPKLLGSCSWEAEGLHCSCSSQASAPSLRWLGLLEGNSSQSFEVT 437
361 VLSLSVHVSPPKLLGSCSWEAEGLHCSCSSQASAPSLRWLGLLEGNSSQSFEVT 420
438 PSSAGPWNSSLSLHGLSSGLRLRCANVHGAQSGSILQPKKGLISTAFSGAFILG 497
421 PSSAGPWNSSLSLHGLSSGLRLRCANVHGAQSGSILQPKKGLISTAFSGAFILG 480
498 IGTALLFLCLALIIWKILPKRTQTETPRPSRHSHTILDYINVVPTAGLAQRNOKA 557

481 IGTALLFLCLALIIWKILPKRTQTETPRPSRHSHTILDYINVVPTAGLAQRNOKA 540
558 TPNSPRTPLPAGAPSPSKKNQKQYQLPSPFPKSKSTQAPESQESQELHYATLNPFGV 617
541 TPNSPRTPLPAGAPSPSKKNQKQYQLPSPFPKSKSTQAPESQESQELHYATLNPFGV 600
618 RPRPEARMPKGTQADYAEVVKFQ 639
601 RPRPEARMPKGTQADYAEVVKFQ 622
RESULT 12
ADD19314
ID ADD19314 standard; protein; 710 AA.
XX
AC ADD19314;
XX
DT 15-JAN-2004 (first entry)
XX Human secreted protein from gene 18 #3.
XX human secreted protein; cytostatic; antibacterial; virucide;
KW neuroprotective; gynaecological; gastrointestinal-Gen; cardiant;
KW cardiovascular-Gen; nephrotropic; anti-inflammatory; muscular-Gen;
KW respiratory-Gen; immunosuppressive; cerebroprotective; vasotropic;
KW neotropic; antiallergic; cancer; bacterial infection; viral infection;
KW neural disorder; immune system disorder; blood disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW inflammatory disorder; proliferative disorder; human.
XX Homo sapiens.
XX WO2003052377-A2.
XX 26-JUN-2003.
XX 06-NOV-2002; 2002WO-US035606.
XX 07-NOV-2001; 2001US-0331046P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2003-533050/50.
XX N-PSDB; ADD19239.
XX New isolated nucleic acids encoding signal transduction pathway component
xx polypeptides, useful for diagnosing, treating, and/or preventing
xx disorders, such as cancer, infections, cardiovascular and inflammatory
xx diseases.
XX Claim 11; SEQ ID NO 141; 554pp; English.
XX The invention relates to an isolated nucleic acid molecule (cDNA)
xx encoding a human secreted protein, representing one of 85 novel genes.
xx Also included are recombinant vectors, host cells (expressing the
xx protein), the secreted proteins (including their fragments, epitopes and
xx homologues), an isolated antibody that binds specifically to the protein,
xx diagnosing a pathological condition or susceptibility to a pathological
xx condition (comprising determining the presence or absence of a mutation
xx in the nucleic acid and diagnosing a condition based on the presence or
xx absence of the mutation), diagnosing a pathological condition or
xx susceptibility to a pathological condition (comprising determining the
xx presence or amount of expression of the protein in a biological sample
xx and diagnosing a condition based on the presence or amount of expression
xx of the protein), preventing, treating or ameliorating a medical condition
xx by administering the nucleic acid or protein to a mammalian subject,
xx identifying a binding partner to the protein, the gene corresponding to
xx the cDNA sequence, and identifying an activity in a biological assay
xx (comprising expressing the nucleic acid in a cell, isolating the

CC supernatant, detecting an activity in a biological assay and identifying
CC the protein in the supernatant having the activity). The nucleic acids
CC and proteins display the following activities: Cytostatic, antibacterial,
CC Virucide, Neuroprotective, Gynaecological, Gastrointestinal-Gen,
CC Cardiac, Cardiovascular-Gen, Nephrotropic, Antiinflammatory, Muscular-
CC Respiratory-Gen, Immunosuppressive, Cerebroprotective, Vasotropic,
CC Nootropic, Antiallergic. The methods and compositions of the present
CC invention are useful for diagnosing, treating, preventing and/or
CC investigating disorders related to the novel polypeptides, such as
CC cancer, bacterial or viral infections, and neural, immune system, blood,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, inflammatory or proliferative disorders (many examples of these
CC diseases and disorders are given in the specification). The present
CC sequence represents a novel secreted protein of the invention.
XX
SQ Sequence 710 AA;

Query Match 94.0%; Score 3174.5; DB 7; Length 710;
Best Local Similarity 89.4%; Pred. No. 7.6e-218; Indels 61; Gaps 2;
Matches 610; Conservative 2; Mismatches 9;
QY 19 GRFWIRVQESVMVPE---GLCISVPCSFSPYPRQDWGTGTPAYGWFKAIVTTTKGAPVAT 75
Db 29 GYGWILDTSGVSDGAGGLCISVPCSFSPYPRQDWGTGTPAYGWFKAIVTTTKGAPVAT 88
QY 76 NHQSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRVERGSYRYNFMNDGF 135
Db 89 NHQSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRVERGSYRYNFMNDGF 148
QY 136 FLKVT----- 140
Db 149 FLKVTALTKQDPVITPEILEPGQPVTVICVFNWAFEECPFPFSFWSGTGAALSQGTKTTS 208
QY 141 ---VLSTFRPDNDHTDITCHVDFSRKGVSAQRTVRLRVAVAPRDLVISRDNTPALEP 197
Db 209 HPSVLSFTPRPDNDHTDITCHVDFSRKGVSAQRTVRLRVAVAPRDLVISRDNTPALEP 268
QY 198 QCGNVPLEAKGQFLLCADSOBPATLSWVLQNEVLSSSHWPGRPLGLELPGVKA 257
Db 269 QCGNVPLEAKGQFLLCADSOBPATLSWVLQNEVLSSSHWPGRPLGLELPGVKA 328
QY 258 GDSGRYTCRAENRSGQRAQLDLSVQYPPENLRVMVMSQANRTVLENLGNGLSLPVLGQS 317
Db 329 GDSGRYTCRAENRSGQRAQLDLSVQYPPENLRVMVMSQANRTVLENLGNGLSLPVLGQS 388
QY 318 LCLVCVTHSSPPARLSWTORGVLSPSPQSPDGVLELPRVQVEHEGFTCHARHPLGSOH 377
Db 389 LCLVCVTHSSPPARLSWTORGVLSPSPQSPDGVLELPRVQVEHEGFTCHARHPLGSOH 448
QY 378 VLSLSVHYSPKLLGFCSCWEAEGHLCSCSQASPAFLRWLGBELLEGNSQDSFVET 437
Db 449 VLSLSVHYSPKLLGFCSCWEAEGHLCSCSQASPAFLRWLGBELLEGNSQDSFVET 508
QY 438 PSSAGFWANSSLSLHGLSSGLRLRCEAWNVHGAQSGILQLPKKKGLISTAFNGAPLG 497
Db 509 PSSAGFWANSSLSLHGLSSGLRLRCEAWNVHGAQSGILQLPKKKGLISTAFNGAPLG 568
QY 498 IGITALLFLCLALITMKILPKERTOTETPRFRFSRHSITLDYINVVPTAGPLAKRNOKA 557
Db 569 IGITALLFLCLALITMKILPKERTOTETPRFRFSRHSITLDYINVVPTAGPLAKRNOKA 628
QY 558 TNSPRTPLPPGAPSPESKKNQKQYQLPSPFPKSSSTQAPESQSOBELHYATLNFPGV 617
Db 629 TNSPRTPLPPGAPSPESKKNQKQYQLPSPFPKSSSTQAPESQSOBELHYATLNFPGV 688
QY 618 RRPPEARPKGTQADYAEVKFQ 639
Db 689 RRPPEARPKGTQADYAEVKFQ 710

RESULT 13
AAU87074
ID AAU87074 standard; protein; 544 AA.

XX AAU87074;
XX AC
XX DT 05-JUN-2002 (first entry)
XX DE Sialic acid-binding Ig-related lectin, Siglec-BMS-13a.
XX KW Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
XX KW immune system disease; leukaemia; allergy; inflammatory disease;
XX KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
XX KW psoriasis; rheumatoid arthritis; conjunctivitis.
XX OS Homo sapiens.
XX PN WO200208257-A2.
XX PD 31-JAN-2002.
XX PF 20-JUL-2001; 2001WO-US023082.
XX PR 21-JUL-2000; 2000US-0220139P.
XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX PI Longphre M, Chang H, Whitney G;
XX DR WPI; 2002-241565/29.
XX DR N-PSDB; ABK43360.
XX PT Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
XX molecules useful for treating immune system diseases such as asthma,
XX leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
XX PS Claim 5; Fig 2B; 209pp; English.
XX CC The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
XX related lectin) protein (I). Pharmaceutical compositions comprising (I)
XX are useful for treating immune system diseases such as asthma, leukaemia
XX or other allergic or inflammatory diseases. Extracellular domains of (I)
XX represent potential markers for screening, diagnosis, prognosis, follow
XX up assays, and imaging methods. (I) is useful as a target for drugs which
XX inhibit inflammation, tissue damage and remodeling in asthma, and
XX inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
XX disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
XX also useful for monitoring the course of disease or disorders, and for
XX identifying agents that bind with and/or modulate the biological activity
XX of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
XX useful in diagnosis and/or prognosis methods, and to detect the presence
XX and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS
XX proteins in a biological sample. (II) are useful as nucleic acid probes
XX are useful for screening genomic library to isolate a genomic clone of
XX SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
XX diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
XX The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
XX expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
XX AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
XX invention
XX SQ Sequence 544 AA;

Query Match 83.0%; Score 2803.5; DB 5; Length 544;
Best Local Similarity 85.1%; Pred. No. 1.7e-191;
Matches 544; Conservative 0; Mismatches 0; Indels 95; Gaps 1;
QY 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWGTGTPAYGW 60
Db 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWGTGTPAYGW 60
QY 61 FKAVTTETTKGAPVATNHQSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
Db 61 FKAVTTETTKGAPVATNHQSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
QY 121 ERGSYRYNFMNDGFLLKVTITVLSFTPRPDNDHTDITCHVDFSRKGVSAQRTVRLRVAVAP 180


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121 ERGSYRVNFMNDGFLKVTLSFTPRPODHTDILTCVDFSRKGVSAQRTVRLVAYAP 180
181 RLIVISISDNTPALPQGGVNPVLEAQKGFLRLCAADSPQATLSWLQNRVLSSS 240
181 RLIVISISDNTPALPQGGVNPVLEAQKGFLRLCAADSPQATLSWLQNRVLSSS 240
241 HPWGPRLGLELPGVKAGSDGRYTCAENRLGSGQALDLSVQYPPENLRVWVSQANRTV 300
241 HPWGPRLGLELPGVKAGSDGRYTCAENRLGSGQALDLSVQYPPENLRVWVSQANRTV 300
301 LENLGNCTSLPVLQSGSLVCTVTHSSPPARLSWTORGQVLSPPSPGVLLEPRVQVE 360
301 LENLGNCTSLPVLQSGSLVCTVTHSSPPARLSWTORGQVLSPPSPGVLLEPRVQVE 360
361 HEGEFTCHARHPLGSHVLSVHSPKXILGPGSCWEAEGLHCSQASGAPSLRWL 420
361 HEGEFTCHARHPLGSHVLSVHSPKXILGPGSCWEAEGLHCSQASGAPSLRWL 420
421 GEELEGNSQDSFEVTPSSAGPWNSSLSLHGLSSGLRLCEANNVHGAQSGSILQLP 480
387 ----- 386
481 DKKGLISTAFSNGAFIGITALLFLCLALIMKILPKRTOTETPRFRSHSTILDYI 540
387 -KKGLISTAFSNGAFIGITALLFLCLALIMKILPKRTOTETPRFRSHSTILDYI 445
541 NVVPTAGPLAQKNOKATNSPRTPLPGCAPSPESKKNQKQYQLPSPEPKSSTQAPES 600
446 NVVPTAGPLAQKNOKATNSPRTPLPGCAPSPESKKNQKQYQLPSPEPKSSTQAPES 505
601 QBSQELHYATLNEPCVRPEARMKPGTQADYAEVKQ 639
506 QBSQELHYATLNEPCVRPEARMKPGTQADYAEVKQ 544

RESULT 14
AAV41724
ID AAY41724 standard; protein; 544 AA.
XX AC AAY41724;
XX AC AAY41724;
XX D7 07-DEC-1999 (first entry)
XX DE Human PRO940 protein sequence.
XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX KW secreted protein; transmembrane protein.
XX OS Homo sapiens.
XX PN WO9946281-A2.
XX XX 16-SEP-1999.
XX XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-0040220.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
27-MAR-1998; 98US-0079689P.
27-MAR-1998; 98US-0079728P.
27-MAR-1998; 98US-0079786P.
30-MAR-1998; 98US-0079920P.
30-MAR-1998; 98US-0079923P.
31-MAR-1998; 98US-0080105P.
31-MAR-1998; 98US-0080107P.
31-MAR-1998; 98US-0080165P.
31-MAR-1998; 98US-0080194P.
01-APR-1998; 98US-0080327P.
01-APR-1998; 98US-0080328P.
01-APR-1998; 98US-0080333P.
01-APR-1998; 98US-0080334P.
08-APR-1998; 98US-0081049P.
08-APR-1998; 98US-0081070P.
08-APR-1998; 98US-0081071P.
09-APR-1998; 98US-0081195P.
09-APR-1998; 98US-0081203P.
09-APR-1998; 98US-0081229P.
15-APR-1998; 98US-0081817P.
15-APR-1998; 98US-0081838P.
15-APR-1998; 98US-0081952P.
15-APR-1998; 98US-0081955P.
21-APR-1998; 98US-0082568P.
21-APR-1998; 98US-0082569P.
22-APR-1998; 98US-0082700P.
22-APR-1998; 98US-0082704P.
22-APR-1998; 98US-0082804P.
23-APR-1998; 98US-0082767P.
23-APR-1998; 98US-0082796P.
27-APR-1998; 98US-0083336P.
28-APR-1998; 98US-0083322P.
29-APR-1998; 98US-0083392P.
29-APR-1998; 98US-0083495P.
29-APR-1998; 98US-0083496P.
29-APR-1998; 98US-0083499P.
29-APR-1998; 98US-0083500P.
29-APR-1998; 98US-0083545P.
29-APR-1998; 98US-0083554P.
29-APR-1998; 98US-0083558P.
29-APR-1998; 98US-0083599P.
30-APR-1998; 98US-0083742P.
05-MAY-1998; 98US-0084366P.
06-MAY-1998; 98US-0084414P.
06-MAY-1998; 98US-0084415P.
07-MAY-1998; 98US-0084598P.
07-MAY-1998; 98US-0084600P.
07-MAY-1998; 98US-0084627P.
07-MAY-1998; 98US-0084637P.
07-MAY-1998; 98US-0084639P.
07-MAY-1998; 98US-0084640P.
07-MAY-1998; 98US-0084643P.
13-MAY-1998; 98US-0085323P.
13-MAY-1998; 98US-0085338P.
15-MAY-1998; 98US-0085339P.
15-MAY-1998; 98US-0085573P.
15-MAY-1998; 98US-0085579P.
15-MAY-1998; 98US-0085580P.
15-MAY-1998; 98US-0085582P.
15-MAY-1998; 98US-0085689P.
15-MAY-1998; 98US-0085697P.
15-MAY-1998; 98US-0085700P.
15-MAY-1998; 98US-0085704P.
22-MAY-1998; 98US-0086023P.
22-MAY-1998; 98US-0086392P.
22-MAY-1998; 98US-0086414P.
22-MAY-1998; 98US-0086430P.
22-MAY-1998; 98US-0086486P.
28-MAY-1998; 98US-0087098P.
28-MAY-1998; 98US-0087106P.
28-MAY-1998; 98US-0087208P.
30-JUL-1998; 98US-0094651P.
11-SEP-1998; 98US-0100038P.
```

XX (GETH) GENENTECH INC.
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI: 1999-551358/46.
DR N-PSDB; AA234109.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
XX Claim 12; Fig 93; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AA233891 to AA234338, and AA41685 to
CC AA41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
SQ Sequence 544 AA;
Query Match 82.6%; Score 2790.5; DB 2; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.4e-190;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;
QY 1 MLLPLLSSLLGGSQAMGRFIRVOESVMVEGLICISVPCSFSPROQDWTGSTPAYGYW 60
DB 1 MLLPLLSSLLGGSQAMGRFIRVOESVMVEGLICISVPCSFSPROQDWTGSTPAYGYW 60
QY 61 FFAVTTETTKGAVATNHQSRVEMSTRGRFQLTGPAGKNCGLVTRDAQMDQESQYFVRV 120
DB 61 FFAVTTETTKGAVATNHQSRVEMSTRGRFQLTGPAGKNCGLVTRDAQMDQESQYFVRV 120
QY 121 ERGSVYRVNFMNDGFFLVKTVLSFTFPRQDHTDLTCHVDFSRKGVSAQRTVRLVAVAP 180
DB 121 ERGSVYRVNFMNDGFFLVKTVLSFTFPRQDHTDLTCHVDFSRKGVSAQRTVRLVAVAP 180
QY 181 RDLVISISRDNTPALEPOQGNVPYLEAKQGFLLCAADSPATLSWLQNRVLSSS 240
DB 181 RDLVISISRDNTPALEPOQGNVPYLEAKQGFLLCAADSPATLSWLQNRVLSSS 240
QY 241 HPWGRPRPLGLELPVKGAGDSGRYTCAENRLGSGQQRALDLSVQYPPENLRVWVSAQRTV 300
DB 241 HPWGRPRPLGLELPVKGAGDSGRYTCAENRLGSGQQRALDLSVQYPPENLRVWVSAQRTV 300
QY 301 LENLNGTSLPYLEGQSLCLVCTHSSPPARLSWTQRCQVLSQSPSPDPGVLELPRVQVE 360
DB 301 LENLNGTSLPYLEGQSLCLVCTHSSPPARLSWTQRCQVLSQSPSPDPGVLELPRVQVE 360
QY 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGFCSCWAEGLHCSQSPAPSLRWL 420
DB 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGFCSCWAEGLHCSQSPAPSLRWL 420
QY 421 GEELEGNSSQDSFEVTPSSAGFWANSSLSLHGLSSGLRLRCEAWNVHGAQSGSILQLP 480
DB 421 GEELEGNSSQDSFEVTPSSAGFWANSSLSLHGLSSGLRLRCEAWNVHGAQSGSILQLP 480
QY 481 DKKGLISTAFNGAFILGIGITALLFCLALIIIMKILPKRTQTEPRFRFHSHTILDIYI 540
DB 481 DKKGLISTAFNGAFILGIGITALLFCLALIIIMKILPKRTQTEPRFRFHSHTILDIYI 540
QY 541 NVVPTAGPLAQRNOKATNSPRTLPAGAPSPESKQKQKQYQLPSPPEPKSSQAPES 600
DB 541 NVVPTAGPLAQRNOKATNSPRTLPAGAPSPESKQKQKQYQLPSPPEPKSSQAPES 600
QY 601 QESQSELHYATLNFPGVRPEARMKPGTQADYAEVKFQ 639
DB 601 QESQSELHYATLNFPGVRPEARMKPGTQADYAEVKFQ 639

Db 506 QESQSELHYATLNFPGVRPEARMKPGTQADYAEVKFQ 544
RESULT 15
AAB44280
XX ID AAB44280 standard; protein; 544 AA.
XX AC AAB44280;
XX 08-FEB-2001 (first entry)
XX Human PRO940 (UNQ477) protein sequence SEQ ID NO:259.
XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
XX expressed sequence tag; detection; cancer.
XX Homo sapiens.
XX WO2000053756-A2.
XX 14-SEP-2000.
XX 18-FEB-2000; 2000WO-US004341.
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 99US-0123957P.
XX 21-MAR-1999; 99US-0126773P.
XX 21-APR-1999; 99US-0130232P.
XX 28-APR-1999; 99US-0131445P.
XX 14-MAY-1999; 99US-0134287P.
XX 23-JUN-1999; 99US-0141037P.
XX 26-JUL-1999; 99US-0145698P.
XX 29-OCT-1999; 99US-0162506P.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 16-DEC-1999; 99WO-US028565.
XX 30-DEC-1999; 99WO-US030095.
XX 05-JAN-2000; 2000WO-US031274.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen WE;
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI: 2000-611443/58.
XX N-PSDB; AAC78510.
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
XX target bioactive molecules to specific cells, and to modulate cellular
XX activities.
XX Claim 12; Fig 93; 636pp; English.
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
XX tag) sequences which encode secreted or transmembrane PRO polypeptides.
XX The PRO polynucleotides and polypeptides have cytostatic activity. The
XX polynucleotides and polypeptides can be used for detecting the presence
XX of PRO polypeptides in samples, for linking bioactive molecules to cells
XX and for modulating biological activities of cells, using the polypeptides
XX for specific targeting. The polypeptide targeting can be used to kill the
XX target cells, e.g. for the treatment of cancers. The polypeptide pairs
XX provide specific targeting of bioactive molecules to cells. AAC78600 to
XX AAC78987 represent PCR primers and probes used in the isolation of the
XX PRO polynucleotide sequences
XX Sequence 544 AA;

Query Match 82.6%; Score 2790.5; DB 3; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.4e-190;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;

QY 1 MLLPLLLSSLLGGSQAMGRFIRVQESVWVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
DB 1 MLLPLLLSSLLGGSQAMGRFIRVQESVWVPEGLCISVPCSFSPRODWTGSTPAYGYW 60

QY 61 FKAVTETTKGAPVATNHQREVEMSTRGRFQLTGDPKCNCSLVIRDAQMDESQYFFRV 120
DB 61 FKAVTETTKGAPVATNHQREVEMSTRGRFQLTGDPKCNCSLVIRDAQMDESQYFFRV 120

QY 121 ERGSYVRYFMNDGFTLVTVLSFTPRQDHNNTDLTCHVDPSRKGVSQRTVRLVAYAP 180
DB 121 ERGSYVRYFMNDGFTLVTVLSFTPRQDHNNTDLTCHVDPSRKGVSQRTVRLVAYAP 180

QY 181 RDLVISISRDNTPALEPQPGNVFYLEAQKGQFLRLCAADSQPPATLSWVLQNEVLSSS 240
DB 181 RDLVISISRDNTPALEPQPGNVFYLEAQKGQFLRLCAADSQPPATLSWVLQNEVLSSS 240

QY 241 HPWGPRLGLPLGVKAGDSGRYTCRAENRGLSQORALDLSVOYPPENLRVWVSQANRTV 300
DB 241 HPWGPRLGLPLGVKAGDSGRYTCRAENRGLSQORALDLSVOYPPENLRVWVSQANRTV 300

QY 301 LENLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGQVLSPOFSDPGVLELPRVQVE 360
DB 301 LENLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGQVLSPOFSDPGVLELPRVQVE 360

QY 361 HECEFTCHARHPLGSHVSLSLSVHYSPKLLGPSCSWEAEGLHCSQSQAAPSRLRWL 420
DB 361 HECEFTCHARHPLGSHVSLSLSVHYSPKLLGPSCSWEAEGLHCSQSQAAPSRLRWL 420

QY 421 GEELLEGNSQDSFEVTPSSAGFWANSLSLHGLSSGLRLRCEAWNVHGAQSGSILQLP 480
DB 387 ----- 386

QY 481 DKKGLISTAFSNGAFIGITALLFLCLALIIIMKILPKERTQETPRPRFSRHSTILDYI 540
DB 387 -KKGLISTAFSNGAFIGITALLFLCLALIIIMKILPKERTQETPRPRFSRHSTILDYI 445

QY 541 NVVPTAGPLAOKENOKATNSPRTPLPGAPSPESKKNOKKQYQLPSPEPKSSTOAPES 600
DB 446 NVVPTAGPLAOKENOKATNSPRTPLPGAPSPESKKNOKKQYQLPSPEPKSSTOAPES 505

QY 601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639
DB 506 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 544

Search completed: November 5, 2004, 13:53:24
Job time : 76.3927 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 74.3927 Seconds
(without alignments)
3081.324 Million cell updates/sec

Title: US-09-937-636-4
Perfect score: 3377
Sequence: 1 MLFLLLSLLGGSQAMGDR.....RPEARMKGTQADYAEVKFQ 639

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3377	100.0	639	2 AAW81023	AAW81023 Human sia
2	3377	100.0	639	3 AAY97543	AAY97543 Human obe
3	3354	99.3	639	3 AAB25580	AAB25580 CD33-like
4	3354	99.3	639	6 ADA27052	ADA27052 Human nov
5	3354	99.3	639	8 ADE85582	ADE85582 Novel hum
6	3338	98.8	697	5 AAU87087	AAU87087 Sialic ac
7	3334	98.7	697	6 ADA27153	ADA27153 Human nov
8	3334	98.7	697	7 ADD26582	ADD26582 Siglec-10
9	3334	98.7	697	8 ADI37010	ADI37010 Novel hum
10	3334	98.7	697	8 ADL82805	ADL82805 Human PRO
11	3299	97.7	622	5 AAU87075	AAU87075 Sialic ac
12	3174.5	94.0	710	7 ADD19314	ADD19314 Human sec
13	2803.5	83.0	544	5 AAU87074	AAU87074 Sialic ac
14	2790.5	82.6	544	2 AAY41724	AAY41724 Human PRO
15	2790.5	82.6	544	3 AAB44280	AAB44280 Human PRO
16	2790.5	82.6	544	4 AAU29082	AAU29082 Human PRO
17	2790.5	82.6	544	6 ABU58458	ABU58458 Human PRO
18	2790.5	82.6	544	6 ABU88006	ABU88006 Novel hum
19	2790.5	82.6	544	6 ABU84321	ABU84321 Human sec
20	2790.5	82.6	544	6 ABR61195	ABR61195 Human sec
21	2790.5	82.6	544	6 ABR65585	ABR65585 Human sec
22	2790.5	82.6	544	6 ABU95525	ABU95525 Human sec
23	2790.5	82.6	544	6 ABU82764	ABU82764 Human PRO
24	2790.5	82.6	544	6 ABU89885	ABU89885 Novel hum
25	2790.5	82.6	544	6 ABR68134	ABR68134 Human sec

ALIGNMENTS

RESULT 1

AAW81023
ID AAW81023 standard; protein; 639 AA.

XX AC AAW81023;

DT 26-APR-1999 (first entry)

DE Human sialoadhesin family 4 (SAF-1) polypeptide.

XX SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer;
KW inflammation; autoimmune disease; allergy; asthma; inflammation;
KW cerebellar degeneration; Alzheimer's disease; Parkinson's disease;
KW multiple sclerosis; amyotrophic lateral sclerosis; head injury;
KW septic shock; sepsis; stroke; osteoporosis; osteoarthritis;
KW ischemia reperfusion injury; cardiovascular disease; kidney disease;
KW liver disease; myocardial infarction; hypotension; hypertension; AIDS;
KW myelodysplastic syndrome; aplastic anaemia; baldness; infection.
XX OS Homo sapiens.

XX WO9853840-A1.

XX 03-DEC-1998.

XX 27-MAY-1998; 98WO-US010791.

XX 27-MAY-1997; 97US-0047572P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Kikly KK, Erickson-Miller CL;

XX WPI; 1999-080779/07.

XX N-PSDB; AAV99911.

PT New sialoadhesin family 4 polypeptides and polynucleotides - useful to treat various diseases associated with SAF-4 expression.

XX Claim 1; Page 31; 48pp; English.

XX This is the amino acid sequence of new human sialoadhesin family 4 (SAF-4), as deduced from the nucleotide sequence of an isolated cDNA clone (see AAV99911). SAF-4 polynucleotides and polypeptides, and methods for producing such polypeptides in transformed host cells using recombinant techniques are disclosed. SAF-4, its agonists and antagonists, and nucleic acid molecules that enhance or inhibit SAF-4 expression, may be used to treat patients in need of enhancement or inhibition of SAF-4

26 2790.5 82.6 544 6 ABU96187 Novel hum
27 2790.5 82.6 544 6 ABU92618 Human sec
28 2790.5 82.6 544 6 ABO08695 Human sec
29 2790.5 82.6 544 6 ABO02747 Human sec
30 2790.5 82.6 544 6 ABR74901 Human sec
31 2790.5 82.6 544 6 ABR94663 Human sec
32 2790.5 82.6 544 6 ABO25226 Novel hum
33 2790.5 82.6 544 6 ABU85636 Human PRO
34 2790.5 82.6 544 6 ABU98796 Novel hum
35 2790.5 82.6 544 6 ABU98011 Novel hum
36 2790.5 82.6 544 6 ABU91717 Novel hum
37 2790.5 82.6 544 6 ABU72332 Novel hum
38 2790.5 82.6 544 6 ABU89410 Human PRO
39 2790.5 82.6 544 6 ABU8251 Human sec
40 2790.5 82.6 544 6 ABU67464 Human sec
41 2790.5 82.6 544 6 ABU80492 Human PRO
42 2790.5 82.6 544 6 ABR99410 Human sec
43 2790.5 82.6 544 6 ABR98800 Human sec
44 2790.5 82.6 544 6 ABO16323 Human sec
45 2790.5 82.6 544 6 ABR92223 Human sec

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expression or activity. Conditions that may benefit from such treatment include cancer, inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury damage and other neurological disorders, septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemia reperfusion injury, cardiovascular disease, kidney disease, liver disease, ischemic injury, myocardial infarction, hypotension, hypertension, AIDS, myelodysplastic syndromes and other hematologic abnormalities, aplastic anaemia, male baldness pattern and bacterial, protozoal, fungal and viral infections related to SAF-4 polypeptide activity. Methods of identifying agonists, antagonists/inhibitors are also provided, as well as diagnostic assays for detecting diseases associated with inappropriate SAF-4 activity or levels

XX Sequence 639 AA;

Query Match: 100.0%; Score 3377; DB 2; Length 639;
 Best Local Similarity 100.0%; Pred. No. 2.3e-232;
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLPLLSSLLGGSQAMDGFWIRVQESVMVPEGLCISVPCSFSPRODWTGSTPAYGW 60
 Db 1 MLLPLLSSLLGGSQAMDGFWIRVQESVMVPEGLCISVPCSFSPRODWTGSTPAYGW 60
 QY 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 Db 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSKGVSAQTVLRYAYAP 180
 Db 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSKGVSAQTVLRYAYAP 180
 QY 181 RDLVISIRSDNTALPAPQPCGNVPYLEAKGQFLRLLCADSPATLSVQLNRVLSS 240
 Db 181 RDLVISIRSDNTALPAPQPCGNVPYLEAKGQFLRLLCADSPATLSVQLNRVLSS 240
 QY 241 HPWGPRPLGLELPGVKGAGSGRYTCRAENRKGSCQALDLSVQYPPENLRVMVQANRTV 300
 Db 241 HPWGPRPLGLELPGVKGAGSGRYTCRAENRKGSCQALDLSVQYPPENLRVMVQANRTV 300
 QY 301 LENLNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGQVLSFQSDPGVLELPRVQVE 360
 Db 301 LENLNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGQVLSFQSDPGVLELPRVQVE 360
 QY 421 GBELLEGNSSQDSFEVTPSAGPWANSSLSHGGSSGLRLRCEAWNVHGAQSGSILQLP 480
 Db 421 GBELLEGNSSQDSFEVTPSAGPWANSSLSHGGSSGLRLRCEAWNVHGAQSGSILQLP 480
 QY 481 DKKGLISTAFSNGAFILGIGITALLFLCLALIMKILPKRRTOTETPRPFRSHSTILDYI 540
 Db 481 DKKGLISTAFSNGAFILGIGITALLFLCLALIMKILPKRRTOTETPRPFRSHSTILDYI 540
 QY 541 NVVPTAGPLAQNQKATNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSSSQAPES 600
 Db 541 NVVPTAGPLAQNQKATNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSSSQAPES 600
 QY 601 QESQBELHVTATLNFPGVRPRPBARMEKGTQADYAEVKFQ 639
 Db 601 QESQBELHVTATLNFPGVRPRPBARMEKGTQADYAEVKFQ 639

RESULT 2

AA97543

ID AA97543 standard; protein; 639 AA.

XX AA97543;

AC AA97543;

XX 12-FEB-2001 (first entry)

XX Human obesity protein binding protein-2 homologue #2.
 DE Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
 XX obesity-related disorder; therapy.
 KW Homo sapiens.
 OS WC200059942-A2.
 PN 12-OCT-2000.
 XX 22-MAR-2000; 2000WO-US006682.
 PP 02-APR-1999; 99US-0127667P.
 XX (ELIL) LILLY & CO ELI.
 PA Su EW, Wei J;
 PI WPI; 2000-664992/64.
 XX N-PSDB; AAA37848.
 DR New human obesity protein binding protein-2 homologue nucleic acids,
 PT polynucleotides and polypeptides useful for producing medicament for
 PT treating obesity and/or obesity-related disorders.
 XX Claim 9; Page 89-91; 92pp; English.

XX This sequence is a human obesity protein binding protein-2 homologue (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h genes or nucleic acids, host cell or tissue in vivo or in vitro.
 CC Antigenic epitope-bearing peptides and polypeptides are useful for
 CC raising or screening antibodies that specifically binds to the hOB-BP2h
 CC polypeptides

XX Sequence 639 AA;

Query Match: 100.0%; Score 3377; DB 3; Length 639;
 Best Local Similarity 100.0%; Pred. No. 2.3e-232;
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLPLLSSLLGGSQAMDGFWIRVQESVMVPEGLCISVPCSFSPRODWTGSTPAYGW 60
 Db 1 MLLPLLSSLLGGSQAMDGFWIRVQESVMVPEGLCISVPCSFSPRODWTGSTPAYGW 60
 QY 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 Db 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSKGVSAQTVLRYAYAP 180
 Db 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSKGVSAQTVLRYAYAP 180
 QY 181 RDLVISIRSDNTALPAPQPCGNVPYLEAKGQFLRLLCADSPATLSVQLNRVLSS 240
 Db 181 RDLVISIRSDNTALPAPQPCGNVPYLEAKGQFLRLLCADSPATLSVQLNRVLSS 240
 QY 241 HPWGPRPLGLELPGVKGAGSGRYTCRAENRKGSCQALDLSVQYPPENLRVMVQANRTV 300
 Db 241 HPWGPRPLGLELPGVKGAGSGRYTCRAENRKGSCQALDLSVQYPPENLRVMVQANRTV 300
 QY 301 LENLNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGQVLSFQSDPGVLELPRVQVE 360
 Db 301 LENLNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGQVLSFQSDPGVLELPRVQVE 360
 QY 361 HEGEFTCHARHPLGSHVLSLSVHSPKLLGPSCSWEAEGHLCSSQASAPSLRWL 420

Query Match	100.0%	Score	1917;	DB	2;	Length	3099;
Best Local Similarity	100.0%	Pred. No.	0;	Mismatches	0;	Indels	0;
Matches	1917;	Conservative	0;	Mismatches	0;	Indels	0;
AAV99912							
ID	AAV99912	standard;	cDNA;	3099	BP.		
XX	AC	AAV99912;					
XX	DT	26-APR-1999	(first entry)				
XX	DE	Human sialoadhesin family 4 (SAF-1)	related EST clone.				
XX	KW	SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer;					
XX	KW	inflammation; autoimmune disease; allergy; asthma; inflammation;					
XX	KW	cellular degeneration; Alzheimer's disease; Parkinson's disease;					
XX	KW	multiple sclerosis; amyotrophic lateral sclerosis; head injury;					
XX	KW	septic shock; sepsis; stroke; osteoporosis; osteoarthritis;					
XX	KW	ischemia reperfusion injury; cardiovascular disease; kidney disease;					
XX	KW	liver disease; myocardial infarction; hypotension; hypertension; AIDS;					
XX	KW	myelodysplastic syndrome; aplastic anaemia; baldness; infection; ss.					
XX	OS	Homo sapiens.					
XX	Key	Location/Qualifiers					
XX	FT	51..1249					
XX	FT	CDS					
XX	FT	/*tag= a					
XX	FT	/transl_except= (pos:1176..1177, aa:Pro)					
XX	FT	/note= "this codon has an apparent 1 nucleotide deletion					
XX	FT	which alters the reading frame"					
XX	PN	W09853840-Al.					
XX	XX						
XX	PD	03-DEC-1998.					
XX	XX						
XX	PF	27-MAY-1998;	98MO-US010791.				
XX	PR	27-MAY-1997;	97US-0047572P.				
XX	PA	(SMIK) SMITHKLINE BEECHAM CORP.					
XX	PI	Kikly KK, Erickson-Miller CL;					
XX	PI	WPI; 1999-080779/07.					
XX	DR	P-PSDB; AA081024.					
XX	XX						
XX	PT	New sialoadhesin family 4 polypeptides and polynucleotides - useful to					
XX	PT	treat various diseases associated with SAF-4 expression.					
XX	PS	Claim 13; Page 31-32; 48pp; English.					
XX	XX						
XX	CC	This is the nucleotide sequence of an expressed sequence tag (EST) clone					
XX	CC	that encodes a polypeptide (see AA081024) which shows close homology					
XX	CC	and/or structural similarity (e.g. a conservative amino acid difference)					
XX	CC	to new human sialoadhesin family 4 (SAF-4) polypeptide (see AA081023).					
XX	CC	SAF-4 polynucleotides and polypeptides, and methods for producing such					
XX	CC	polypeptides in transformed host cells using recombinant techniques, are					
XX	CC	disclosed. SAF-4, its agonists and antagonists, and nucleic acid					
XX	CC	molecules that enhance or inhibit SAF-4 expression, may be used to treat					
XX	CC	patients in need of enhancement or inhibition of SAF-4 expression or					
XX	CC	activity. Conditions that may benefit from such treatment include cancer,					
XX	CC	inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS					
XX	CC	disease, multiple sclerosis, myotrophic lateral sclerosis, head injury					
XX	CC	damage and other neurological disorders, septic shock, sepsis, stroke,					
XX	CC	osteoporosis, osteoarthritis, ischemia reperfusion injury, cardiovascular					
XX	CC	disease, kidney disease, liver disease, ischemic injury, myocardial					
XX	CC	infarction, hypotension, hypertension, AIDS, myelodysplastic syndromes					
XX	CC	and other haematologic abnormalities, aplastic anaemia, male baldness					
XX	CC	pattern and bacterial, protozoal, fungal and viral infections related to					
XX	CC	SAF-4 polypeptide activity. Methods of identifying agonists,					
XX	CC	antagonists/inhibitors are also provided, as well as diagnostic assays					
XX	CC	for detecting diseases associated with inappropriate SAF-4 activity or					
XX	XX	levels					
XX	XX	Sequence 3099 BP; 770 A; 907 C; 813 G; 607 T; 0 U; 2 Other;					

Sequence 3099 BP; 770 A; 907 C; 813 G; 607 T; 0 U; 2 Other;

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